

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 19, 2006, 13:50:01 ; Search time 218.657 Seconds
(without alignments)
753.540 Million cell updates/sec

Title: US-10-799-943-2
Perfect score: 2009
Sequence: 1 MSHKGSVVAQNGAPASNR.....SNLQFRYGLGGCTDITLL 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	4	AAB74699 Human mem
2	2009	100.0	375	4	AAM78650 Human pro
3	2009	100.0	375	5	ABB89913 Human pol
4	2009	100.0	375	8	ADQ37764 Human adi
5	2009	100.0	375	9	ADW24159 Human adi
6	2009	100.0	375	9	ADZ00539 Human adi
7	2005	99.8	379	4	AAM79634 Human pro
8	1998	99.5	375	4	AAB93005 Human pro
9	1970	98.1	370	6	ABB99648 Amino aci
10	1967	97.9	375	9	ADW24313 Rat Adipo
11	1954	97.3	375	8	ADQ37768 Mouse adi
12	1954	97.3	375	9	ADW24160 Murine Ad
13	1696	84.4	387	4	AAU30936 Novel hum
14	1529	76.1	381	9	ADW24251 Human adi
15	1403.5	69.9	386	8	ADRO9023 Human pro
16	1403.5	69.9	386	8	ADRL0196 Human pro
17	1403.5	69.9	386	8	ADG98076 Protein f
18	1403.5	69.9	386	8	ADU76417 Progestin
19	1391.5	69.3	386	9	ADW24156 Murine Ad
20	1378.5	68.6	386	9	ADW24315 Rat Adipo
21	1378	68.6	311	8	ADQ37770 Mouse adi
22	1378	68.6	311	9	ADW24162 Murine Ad
23	1378	68.6	311	9	ADW24397 Murine Ad
24	1376	68.5	421	9	ADW24253 Human Adi

25	1359	67.6	386	9	ADW24154 Human Adi
26	1347	67.0	299	8	ADQ37766 Human adi
27	1345	66.9	299	8	ADW24161 Human Adi
28	1344	66.9	299	6	ABO01308 Human pro
29	1291	64.3	299	8	ADN95988 Human NOV
30	1121	55.8	258	8	ABB99647 Amino aci
31	1121	55.8	258	8	ADU06670 Novel bro
32	1121	55.8	258	9	ADZ09443 Human Adi
33	1117	55.6	258	4	AAM79290 Human pro
34	1075	53.5	201	6	ADA57272 Human sec
35	1075	53.5	201	6	ADA41153 Human sec
36	1075	53.5	201	7	ADC74358 Human sec
37	1075	53.5	201	7	ADD37995 Human sec
38	1075	53.5	201	7	ADE11759 Human sec
39	1075	53.5	201	3	AAI76136 Human sec
40	1052.5	52.4	288	6	ABB99649 Amino aci
41	1052.5	52.4	288	9	ADW24158 Human Adi
42	1016.5	50.6	444	4	ABB61417 Drosophil
43	1001.5	49.9	322	4	ABB66248 Drosophil
44	928	46.2	218	4	AAM80274 Human pro
45	928	46.2	218	8	ADS98656 Protein f

ALIGNMENTS

RESULT 1
AAB74699
ID AAB74699 standard; protein; 375 AA.
XX
AC AAB74699;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-5.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022315.
XX
PR 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
PA (INCY-) INCYTE GENOMICS INC.
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn NR, Lu DAM, Patterson C;
XX
XX WFI; 2001-168860/17.
XX N-PSDB; AAF81745.
PT Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX
XX Claim 1; Page 118; 173pp; English.
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition

CC associated with decreased expression of functional MEMAP and antagonists
 CC of MEMAP are used to treat a disease or condition associated with
 CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated with
 CC MEMAP
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE 60
 DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE 60
 QY 61 EEEVRVLTLPQAHAMEKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPQAHAMEKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 QY 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTLMLRPNMYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTLMLRPNMYFMAPLQKVVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 DB 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDTL 375

RESULT 2
 AAM78650
 ID AAM78650 standard; protein; 375 AA.
 XX
 AC AAM78650;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1312.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX
 PN W0200157190-A2.
 XX
 PD 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren P, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51783.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 3561-3562; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE 60
 DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE 60
 QY 61 EEEVRVLTLPQAHAMEKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPQAHAMEKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 QY 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTLMLRPNMYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTLMLRPNMYFMAPLQKVVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 DB 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDTL 375

RESULT 3
 ID ABB89913 standard; protein; 375 AA.
 XX ABB89913;
 AC ABB89913;
 DT 24-MAY-2002 (first entry)
 XX Human polypeptide SEQ ID NO 2289.
 DE
 DE
 DE
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 19-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-122018/16.
 DR N-PSDB; ABL90322.
 DR
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 XX Claim 11; SEQ ID NO 2289; 2081pp + Sequence Listing; English.
 XX
 XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 375 AA;
 XX
 Query Match 100.0%; Score 2009; DB 5; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVQAQNGAPASREADTVLAEGLPGLLEEKGRKRVIANPPKAESEQCPVPQEE 60
 DB 1 MSHKGSVQAQNGAPASREADTVLAEGLPGLLEEKGRKRVIANPPKAESEQCPVPQEE 60
 QY 61 EEEVRVLTPLQAHAMEKMEEFYKVGEGRWVVPYDVLFDMLKONDYLLHGRHPMPS 120
 DB 61 EEEVRVLTPLQAHAMEKMEEFYKVGEGRWVVPYDVLFDMLKONDYLLHGRHPMPS 120

QY 121 FRACEKSIPIRIHTETGNIWTHLLGCVLFLFLGILTMLRPNMYFMAPLOEKVVFGMFFLGA 180
 DB 121 FRACEKSIPIRIHTETGNIWTHLLGCVLFLFLGILTMLRPNMYFMAPLOEKVVFGMFFLGA 180
 QY 181 VLCLSFSLFWLFTVYCHSEKSVRTFSKLDYSGIALLIMGSFVFWLWYFYSCSPQRLIYLS 240
 DB 181 VLCLSFSLFWLFTVYCHSEKSVRTFSKLDYSGIALLIMGSFVFWLWYFYSCSPQRLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHROTGRAGVFLGLGLSGVVPVTHFTIABGFVKATVGM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHROTGRAGVFLGLGLSGVVPVTHFTIABGFVKATVGM 300
 QY 301 GHFFFLMVMYITGAGLYAARIEREPFGKFDIWFQSHQIFHVLVVAAPVHFVGVSNLOE 360
 DB 301 GHFFFLMVMYITGAGLYAARIEREPFGKFDIWFQSHQIFHVLVVAAPVHFVGVSNLOE 360
 QY 361 FRYGLEGGCTDDTLL 375
 DB 361 FRYGLEGGCTDDTLL 375
 RESULT 4
 ADQ37764
 ID ADQ37764 standard; protein; 375 AA.
 XX ADQ37764;
 XX 07-OCT-2004 (first entry)
 XX Human adiponectin receptor AdipoR1 protein SEQ ID NO:2.
 DE Human adiponectin receptor; adiponectin binding; human; AdipoR1.
 KW adiponectin receptor; adiponectin binding; human; AdipoR1.
 XX Homo sapiens.
 XX WO2004061108-A1.
 XX 22-JUL-2004.
 XX 12-JUN-2003; 2003WO-JP007515.
 XX 29-DEC-2002; 2002JP-00383738.
 XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX (NISC) NISSAN CHEM IND LTD.
 XX Kadowaki T, Yamauchi T, Nagai R, Kamon J;
 XX WPI; 2004-543879/52.
 XX N-PSDB; ADQ37763.
 XX New protein having adiponectin binding capacity, useful for screening
 PT ligand, agonist or antagonist with respect to adiponectin receptor.
 PT
 PS Claim 1; SEQ ID NO 2; 122pp; Japanese.
 XX The present invention describes an adiponectin receptor protein (I)
 CC having adiponectin binding capacity, and having a sequence of 375, 299,
 CC 375, or 311 amino acids (S1, see SEQ ID NO:2, 4, 6 and 8 (ADQ37764,
 CC ADQ37766, ADQ37768 and ADQ37770)), or a protein which has one or more
 CC amino acid deletion, substitution or addition in (S1). Also described:
 CC (1) a gene (II) encoding (I); (2) a recombinant vector (III) containing
 CC (II); (3) a transformed host (IV) containing (III); (4) an antibody which
 CC reacts with (I) or its fragment; and (5) a kit for screening a ligand, an
 CC agonist or an antagonist with respect to adiponectin receptor, comprising
 CC any one of (I)-(IV). (I) is useful for screening a ligand, an agonist or
 CC an antagonist of adiponectin receptor, which involves contacting the test
 CC substance with (I). The present sequence represents the human adiponectin
 CC receptor AdipoR1, which is used in the exemplification of the present
 CC invention.
 XX Sequence 375 AA;
 XX

Query Match	100.0%;	Score 2009;	DB 8;	Length 375;	
Best Local Similarity	100.0%;	Pred. No. 2.4e-214;			
Matches 375;	Conservative	0;	Mismatches	0;	Indels
QY	1	MSSHKGSVVQAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE	60		
DB	1	MSSHKGSVVQAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQEE	60		
QY	61	EEVRVLTLPLOAHAMEKEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS	120		
DB	61	EEVRVLTLPLOAHAMEKEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS	120		
QY	121	FRACFKSIFRIHTETGNIWTHLLGFVFLFLGILTLMLRNPMYFMAPLQKVFQGMFFLGA	180		
DB	121	FRACFKSIFRIHTETGNIWTHLLGFVFLFLGILTLMLRNPMYFMAPLQKVFQGMFFLGA	180		
QY	181	VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYFYCSPQPLIYLS	240		
DB	181	VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYFYCSPQPLIYLS	240		
QY	241	IVCVLGISAIIVAQWDRFATPKHQRTRAGVFLGLSLGVVPTMHTFIAEGFVKATTVGOM	300		
DB	241	IVCVLGISAIIVAQWDRFATPKHQRTRAGVFLGLSLGVVPTMHTFIAEGFVKATTVGOM	300		
QY	301	GWFFLMAVMYITGAGLYAARIPIERFPCKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE	360		
DB	301	GWFFLMAVMYITGAGLYAARIPIERFPCKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE	360		
QY	361	FRYGLEGGCTDDTL 375			
DB	361	FRYGLEGGCTDDTL 375			
RESULT 5					
ADW24159					
ID	ADW24159	standard; protein; 375 AA.			
XX	AC	ADW24159;			
XX	DT	24-MAR-2005 (first entry)			
XX	DE	Human AdipoR1 (adiponectin receptor 1) protein.			
XX	KW	antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen-;			
XX	KW	cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;			
XX	KW	cytostatic; virucide; antithyroid; metabolic; anabolic;			
XX	KW	eating-disorders-gen.; metabolic disorder; inflammation;			
XX	KW	cardiovascular disease; nutritional disorder; obesity;			
XX	KW	insulin dependent diabetes; non-insulin dependent diabetes;			
XX	KW	insulin resistance; myocardial infarction; cardiac failure;			
XX	KW	atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;			
XX	KW	hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;			
XX	KW	viral infection; AdipoR1; adiponectin receptor 1.			
XX	OS	Homo sapiens.			
XX	PN	WO2005001061-A2.			
XX	PD	06-JAN-2005.			
XX	XX	24-JUN-2004; 2004WO-US020399.			
XX	PF	25-JUN-2003; 2003US-0482324P.			
XX	PR	10-JUL-2003; 2003US-0486036P.			
XX	PR	04-AUG-2003; 2003US-0492470P.			
XX	PR	02-OCT-2003; 2003US-0508225P.			
XX	PR	11-MAR-2004; 2004US-0552084P.			
XX	XX	(BRIM) BRISTOL-MYERS SQUIBB CO.			
XX	PA	Chen J, Wu S, Lee N;			
XX	PI				
XX	XX				

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RESULT 6
ADZ00539
ID ADZ00539 standard; protein; 375 AA.
XX
AC ADZ00539;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human AdipoR1.
XX
KW Cardiant; Dermatological; Gastrointestinal; Hemostatic; Respiratory-Gen;
KW Nootropic; Neuroprotective; Uropathic; Cystostatic; Antiinflammatory;
KW AdipoR1-inhibitor; AdipoR1-activator; G protein coupled receptor;
KW AdipoR1; receptor.
XX
OS Homo sapiens.
XX
PN WO2005031346-A2.
XX
PD 07-APR-2005.
XX
PF 16-SEP-2004; 2004WO-EP010384.
XX
PR 27-SEP-2003; 2003EP-00021897.
XX
PA (FARB ) BAYER HEALTHCARE AG.
XX
PI Golz S, Brueggemeier U, Geerts A;
XX
WPI; 2005-254243/26.
DR N-PSDB; ADZ00538.
XX
PT Screening for therapeutic agents useful for treating cardiovascular,
PT dermatological, respiratory or neurological diseases, cancer or
PT inflammation in a mammal comprises contacting a test compound with a
PT AdipoR1 polypeptide.
XX
PS Disclosure; SEQ ID NO 2; 135pp; English.
XX
CC This sequence represents the G protein coupled receptor, AdipoR1. The
CC method of the invention for screening for therapeutic agents useful for
CC treating cardiovascular, dermatological, gastroenterological,
CC hematological, respiratory, neurological or urological diseases, cancer
CC or inflammation in a mammal comprises contacting a test compound with an
CC AdipoR1 polypeptide and detecting binding of the test compound to the
CC AdipoR1 polypeptide. A further method is included for diagnosing any of
CC the diseases cited above in a mammal comprising determining the amount of
CC an AdipoR1 polynucleotide in a sample taken from the mammal and
CC determining the amount of AdipoR1 polynucleotide in healthy and/or
CC diseased mammals. Regulators of AdipoR1 activity are useful for
CC regulating AdipoR1 activity in a mammal having such diseases.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-214;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHKGSVAQNGAPASREADTVLAEGLPLEEKGRVIANPPKAESEQCPVPQEE 60
DB 1 MSHKGSVAQNGAPASREADTVLAEGLPLEEKGRVIANPPKAESEQCPVPQEE 60
QY 61 EEEVRVLTFLQAHAMKEEFYKVGWGRWRVPIYDVLPDVLTNDYLLHGRPPMPS 120
DB 61 EEEVRVLTFLQAHAMKEEFYKVGWGRWRVPIYDVLPDVLTNDYLLHGRPPMPS 120
QY 121 FRACFKSIFRIHTETGNITWHLGFLVFLFLGILTMLRPNMYFAPLQEKVFGMFLGA 180
DB 121 FRACFKSIFRIHTETGNITWHLGFLVFLFLGILTMLRPNMYFAPLQEKVFGMFLGA 180
QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVCSQPRLIYLS 240
DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVCSQPRLIYLS 240

RESULT 7
AAM79634
ID AAM79634 standard; protein; 379 AA.
XX
AC AAM79634;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3280.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
(HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
WPI; 2001-476283/51.
DR N-PSDB; AAK52767.
XX
Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.
XX
Claim 20; Page 300; 6221pp; English.
XX
The invention relates to polynucleotides (AAK51456-AAK53435) and the
encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and/or
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant sequences from the

```

CC sequence listing were missing at the time of publication

XX Sequence 379 AA;

Query Match 99.8%; Score 2005; DB 4; Length 379;

Best Local Similarity 99.7%; Pred. NO. 6.7e-214;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSHKSVAOAGNGAPASNRADTVLAEGLPILLEKGRVIANPPKAEETCTCPVQEE 60

DB 5 MSSHKSVAOAGNGAPASNRADTVLAEGLPILLEKGRVIANPPKAEETCTCPVQEE 64

QY 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGHRPPMS 120

DB 65 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGHRPPMS 124

QY 121 FRACFKSIFRIHTETGNIWTHLLGFLVFLPLGILTMRLPNMYMAPLQEKVFGMFFLGA 180

DB 125 FRACFKSIFRIHTETGNIWTHLLGFLVFLPLGILTMRLPNMYMAPLQEKVFGMFFLGA 184

QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWYYSFYCSPQPRLIYLS 240

DB 185 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWYYSFYCSPQPRLIYLS 244

QY 241 IVCVLGISAIIVAQWDRFATPKHRQTRAGVFLGLGLSGVVPTMHTFIAGFVKATTVGQM 300

DB 245 IVCVLGISAIIVAQWDRFATPKHRQTRAGVFLGLGLSGVVPTMHTFIAGFVKATTVGQM 304

QY 301 GWFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPFVHFYGVSNLQE 360

DB 305 GWFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPFVHFYGVSNLQE 364

QY 361 FRYGLEGGCTDDTLL 375

DB 365 FRYGLEGGCTDDTLL 379

RESULT 8

AAB93005

ID AAB93005 standard; protein; 375 AA.

XX AAB93005;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:11749.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 28-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isozaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Iehii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-

XX length cDNAs defined in the specification, and for the detection and/or

XX diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX Claim 8; SEQ ID NO 11749; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-

XX length cDNAs defined in the specification. Where a primer set comprises:

XX (a) an oligo-dT primer and an oligonucleotide complementary to the

XX complementary strand of a polynucleotide which comprises one of the 5602

XX nucleotide sequences defined in the specification, where the

XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination

XX of an oligonucleotide comprising a sequence complementary to the

XX complementary strand of a polynucleotide which comprises a 5'-end

XX sequence and an oligonucleotide comprising a sequence complementary to a

XX polynucleotide which comprises a 3'-end sequence, where the

XX oligonucleotide comprises at least 15 nucleotides and the combination of

XX the 5'-end sequence/3'-end sequence is selected from those defined in the

XX specification. The primer sets can be used in antisense therapy and in

XX gene therapy. The primers are useful for synthesizing polynucleotides,

XX particularly full-length cDNAs. The primers are also useful for the

XX detection and/or diagnosis of the abnormality of the proteins encoded by

XX the full-length cDNAs. The primers allow obtaining of the full-length

XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893

XX represent human amino acid sequences; and AAH13629 to AAH13632 represent

XX oligonucleotides, all of which are used in the exemplification of the

XX present invention

XX SQ Sequence 375 AA;

Query Match 99.5%; Score 1998; DB 4; Length 375;

Best Local Similarity 99.7%; Pred. NO. 4e-213;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSHKSVAOAGNGAPASNRADTVLAEGLPILLEKGRVIANPPKAEETCTCPVQEE 60

DB 1 MSSHKSVAOAGNGAPASNRADTVLAEGLPILLEKGRVIANPPKAEETCTCPVQEE 60

QY 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGHRPPMS 120

DB 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGHRPPMS 120

QY 121 FRACFKSIFRIHTETGNIWTHLLGFLVFLPLGILTMRLPNMYMAPLQEKVFGMFFLGA 180

DB 121 FRACFKSIFRIHTETGNIWTHLLGFLVFLPLGILTMRLPNMYMAPLQEKVFGMFFLGA 180

QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWYYSFYCSPQPRLIYLS 240

DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWYYSFYCSPQPRLIYLS 240

QY 241 IVCVLGISAIIVAQWDRFATPKHRQTRAGVFLGLGLSGVVPTMHTFIAGFVKATTVGQM 300

DB 241 IVCVLGISAIIVAQWDRFATPKHRQTRAGVFLGLGLSGVVPTMHTFIAGFVKATTVGQM 300

QY 301 GWFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPFVHFYGVSNLQE 360

DB 301 GWFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPFVHFYGVSNLQE 360

QY 361 FRYGLEGGCTDDTLL 375

DB 361 FRYGLEGGCTDDTLL 375

RESULT 9

AAB99648

ID AAB99648 standard; protein; 370 AA.

XX AAB99648;

XX 28-MAR-2003 (first entry)

XX Amino acid sequence GI7705761 related to FLJ nucleic acids.

XX FLJ; p53 pathway; cancer; G11375715.

XX OS Homo sapiens.
 XX FH Key
 XX Domain Location/Qualifiers
 FT /note= "UPF0073 domain"
 FT 119..356
 FT Domain /note= "transmembrane domain"
 FT 135..157
 FT Domain /note= "transmembrane domain"
 FT 172..194
 FT Domain /note= "transmembrane domain"
 FT 207..226
 FT Domain /note= "transmembrane domain"
 FT 236..255
 FT Domain /note= "transmembrane domain"
 FT 268..287
 FT Domain /note= "transmembrane domain"
 FT 297..319
 FT Domain /note= "transmembrane domain"
 FT 339..356
 FT Domain /note= "transmembrane domain"
 XX WO200298898-A2.
 PN 12-DEC-2002.
 XX
 XX 03-JUN-2002; 2002WO-US017459.
 XX
 XX 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI WPI; 2003-129570/12.
 XX
 XX Identifying FLJ-specific modulating agents useful for diagnosing or
 PT treating disorders associated with defective p53 function, e.g. cancer,
 PT comprises comparing a test agent-biased activity and a reference activity
 PT in an assay.
 XX
 XX Example; Page 52-53; 54pp; English.
 XX
 XX The present sequence represents a polypeptide sequence which is related
 CC to FLJ nucleic acids. Genes that modify the p53 pathway in Drosophila are
 CC referred to as FLJ. The specification describes a method for identifying
 CC candidate p53 pathway modulating agents. The method comprises providing
 CC assay system with purified FLJ polypeptide/nucleic acid or their active
 CC fragment/derivative; contacting the system with test agent where, in the
 CC presence of the agent, the system provides a reference activity; and
 CC detecting test agent-biased activity, where differences between test
 CC agent-biased activity and reference activity identifies a candidate. The
 CC method is useful in identifying a candidate p53 pathway modulating agent,
 CC such as a human FLJ gene, that acts as therapeutic or diagnostic targets
 CC for disorders associated with defective p53 function, such as cancer
 XX
 XX Sequence 370 AA;
 SQ
 Query Match 98.1%; Score 1970; DB 6; Length 370;
 Best Local Similarity 100.0%; Pred. No. 5.2e-210;
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVAAQNGCAPASNREADTVLAEIPLLEKGRVIANPPKAESEQCVPQEE 60
 DB 1 MSHKGSVAAQNGCAPASNREADTVLAEIPLLEKGRVIANPPKAESEQCVPQEE 60
 QY 61 EEEVRVLTLPLOAHAMEKMEEFYKVGEGRRVPIPDVLPDMLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPLOAHAMEKMEEFYKVGEGRRVPIPDVLPDMLKNDYLLHGRPPMPS 120
 QY 121 FRACFKSIFRIHTETGNIWTHLLGFVLFILGILTMLRPNNYFMAPLQEKVFGVGMFFLGA 180

DB 121 FRACFKSIFRIHTETGNIWTHLLGFVLFILGILTMLRPNNYFMAPLQEKVFGVGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPLWLYSYFYCSPQRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPLWLYSYFYCSPQRLIYLS 240
 QY 241 IVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLGSLGVVPTMHFTIARGFVKATTVGOM 300
 DB 241 IVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLGSLGVVPTMHFTIARGFVKATTVGOM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVWAAAFVHFYGVSNLQE 360
 DB 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVWAAAFVHFYGVSNLQE 360
 QY 361 FRYGLEGG 368
 DB 361 FRYGLEGG 368
 RESULT 10
 ADW24313
 ID ADW24313 standard; protein; 375 AA.
 XX
 AC ADW24313;
 XX
 XX 24-MAR-2005 (first entry)
 XX
 XX Rat AdipoR1 (adiponectin receptor 1) protein.
 XX
 XX antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;
 KW cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;
 KW cytostatic; virucide; antithyroid; metabolic; anabolic;
 KW eating-disorders-gen.; metabolic disorder; inflammation;
 KW cardiovascular disease; nutritional disorder; obesity;
 KW insulin dependent diabetes; non-insulin dependent diabetes;
 KW insulin resistance; myocardial infarction; cardiac failure;
 KW atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;
 KW hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;
 KW viral infection; AdipoR1; adiponectin receptor 1.
 XX
 OS Rattus sp.
 XX
 XX WO2005001061-A2.
 XX
 XX 06-JAN-2005.
 XX
 XX 24-JUN-2004; 2004WO-US020399.
 XX
 XX 25-JUN-2003; 2003US-0482324P.
 PR 10-JUL-2003; 2003US-0486036P.
 PR 04-AUG-2003; 2003US-0492470P.
 PR 02-OCT-2003; 2003US-0508225P.
 PR 11-MAR-2004; 2004US-0552084P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX
 XX Chen J, Wu S, Lee N;
 XX
 XX WPI; 2005-075549/08.
 DR N-PSDB; ADW24312.
 XX
 XX New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding
 PT nucleic acid, useful for diagnosing, preventing and/or treating a
 PT disorder related to aberrant adiponectin binding activity and/or
 PT expression.
 XX
 XX Claim 5; SEQ ID NO 165; 469pp; English.
 PS
 XX The invention relates to a novel isolated AdipoRv (adiponectin receptor
 CC splice variant) nucleic acid molecule. Adiponectin
 CC (Acrp30/AdipoQ/apM1/GBP28) is the most abundant adipose-specific hormone
 CC and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-
 CC atherogenic adipokine. The polynucleotide of the invention demonstrates

CC anti-diabetic, antibacterial, anti-arteriosclerotic, cardiovascular-gen.,
 CC cardiant, anti-inflammatory, antilipemic, antibacterial, anorectic,
 CC cytostatic, virucide, antithyroid, metabolic, anabolic and eating-
 CC disorders-gen. activities. The polypeptides and their modulators may be
 CC useful for preventing, treating or ameliorating a disorder selected from
 CC metabolic disorders, inflammatory disorders, cardiovascular disorders,
 CC obesity, diabetes, type I diabetes, type II diabetes, gestational
 CC diabetes, early onset diabetes, insulin resistance, disorders in which
 CC glucose-lowering would be beneficial, disorders in which amelioration of
 CC insulin resistance would be beneficial, disorders in which suppressed FA
 CC influx into liver would be beneficial, disorders in which reduced serum
 CC TG would be beneficial, myocardial infarction, heart failure,
 CC atherosclerosis, arteriosclerosis, disorders associated with aberrant
 CC activity or expression of an adiponectin receptor, disorders associated
 CC with aberrant vascular smooth muscle proliferation, disorders associated
 CC with aberrant foam cell formation, disorders in which inhibition of
 CC macrophage phagocytosis would be beneficial, disorders in which
 CC inhibition of TNF-alpha production would be beneficial, dyslipidemia,
 CC diabetic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,
 CC hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The
 CC polypeptides and polynucleotides can also be used in diagnosing,
 CC preventing and treating cancer, and bacterial or viral infectious
 CC disorders. The current sequence is that of a rat Adiporv (adiponectin
 CC receptor splice variant) protein of the invention.

XX Sequence 375 AA;

Query Match 97.9%; Score 1967; DB 9; Length 375;
 Best Local Similarity 97.6%; Pred. No. 1.1e-209;
 Matches 366; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSHKGSVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEETQCPVQEE 60
 DB 1 MSHKGSVAQNGAPSSNRADTVLAEGLPLEEKGKRAATSPAKAEEOQCPVQEE 60
 QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS 120
 DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS 120
 QY 121 FRACFKSIPIRHTETGNIWTHLLGFLVFLPLGLITMLRPNMYMAPLQEKVFGMFFLGA 180
 DB 121 FRACFKSIPIRHTETGNIWTHLLGFLVFLPLGLITMLRPNMYMAPLQEKVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQPLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQPLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHRTAGVFLGLSLGVVPTMHFTIAGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHRTAGVFLGLSLGVVPTMHFTIAGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITAGLYAARIPIRPPFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEE 360
 DB 301 GWFFLMAVMYITAGLYAARIPIRPPFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEE 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDSL 375

RESULT 11

ID ADQ37768 standard; protein; 375 AA.

XX ADQ37768;

XX 07-OCT-2004 (first entry)

DE Mouse adiponectin receptor AdipoR1 protein SEQ ID NO:6.

XX adiponectin receptor; adiponectin binding; mouse; AdipoR1.

XX Mus musculus.

XX WO2004061108-A1.
 XX 22-JUL-2004.
 PD 12-JUN-2003; 2003WO-JP007515.
 PF 29-DEC-2002; 2002JP-00383738.
 PR (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 PA (NISC) NISSAN CHEM IND LTD.
 XX Kadowaki T, Yamauchi T, Nagai R, Kamon J;
 XX WPI; 2004-543879/52.
 DR N-PSDB; ADQ37767.
 XX New protein having adiponectin binding capacity, useful for screening
 XX ligand, agonist or antagonist with respect to adiponectin receptor.
 PS Claim 1; SEQ ID NO 6; 122pp; Japanese.
 XX The present invention describes an adiponectin receptor protein (I)
 CC having adiponectin binding capacity, and having a sequence of 375, 299,
 CC 375, or 311 amino acids (S1, see SEQ ID NO:2, 4, 6 and 8 (ADQ37764,
 CC ADQ37766, ADQ37768 and ADQ37770)), or a protein which has one or more
 CC amino acid deletion, substitution or addition in (S1). Also described:
 CC (1) a gene (II) encoding (I); (2) a recombinant vector (III) containing
 CC (II); (3) a transformed host (IV) containing (III); (4) an antibody which
 CC reacts with (I) or its fragment; and (5) a kit for screening a ligand, an
 CC agonist or an antagonist with respect to adiponectin receptor, comprising
 CC any one of (I)-(IV). (I) is useful for screening a ligand, an agonist or
 CC an antagonist of adiponectin receptor, which involves contacting the test
 CC substance with (I). The present sequence represents the mouse adiponectin
 CC receptor Adipor1, which is used in the exemplification of the present
 CC invention.

Sequence 375 AA;

Query Match 97.3%; Score 1954; DB 8; Length 375;
 Best Local Similarity 96.8%; Pred. No. 3.2e-208;
 Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSHKGSVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEETQCPVQEE 60
 DB 1 MSHKGSVAQNGAPSGNRADTVLAEGLPLEEKGKRAASSPAKAEEDQACVPQEE 60
 QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS 120
 DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGHPPMPS 120
 QY 121 FRACFKSIPIRHTETGNIWTHLLGFLVFLPLGLITMLRPNMYMAPLQEKVFGMFFLGA 180
 DB 121 FRACFKSIPIRHTETGNIWTHLLGFLVFLPLGLITMLRPNMYMAPLQEKVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQPLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQPLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHRTAGVFLGLSLGVVPTMHFTIAGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHRTAGVFLGLSLGVVPTMHFTIAGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITAGLYAARIPIRPPFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEE 360
 DB 301 GWFFLMAVMYITAGLYAARIPIRPPFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEE 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDSL 375

RESULT 12

ADW24160
ID ADW24160 standard; protein; 375 AA.
XX
XX ADW24160;
XX
XX 24-MAR-2005 (first entry)
XX
XX Murine AdipoR1 (adiponectin receptor 1) protein.
DE
XX
XX antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;
XX cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;
XX cytosolic; virucide; antithyroid; metabolic; anabolic;
XX eating-disorders-gen.; metabolic disorder; inflammation;
XX cardiovascular disease; nutritional disorder; obesity;
XX insulin dependent diabetes; non-insulin dependent diabetes;
XX insulin resistance; myocardial infarction; cardiac failure;
XX atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;
XX hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;
XX viral infection; AdipoR1; adiponectin receptor 1.
XX
XX Mus musculus.
XX
XX W02005001061-A2.
XX
XX 06-JAN-2005.
XX
XX 24-JUN-2004; 2004WO-US020399.
XX
XX 25-JUN-2003; 2003US-048224P.
XX
XX 10-JUL-2003; 2003US-0486036P.
XX
XX 04-AUG-2003; 2003US-0492470P.
XX
XX 02-OCT-2003; 2003US-0508225P.
XX
XX 11-MAR-2004; 2004US-0552084P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Chen J, Wu S, Lee N;
XX
XX WPI; 2005-075549/08.
XX
XX New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding
XX nucleic acid, useful for diagnosing, preventing and/or treating a
XX disorder related to aberrant adiponectin binding activity and/or
XX expression.
XX
XX Disclosure; SEQ ID NO 8; 469pp; English.
XX
XX The invention relates to a novel isolated AdipoRv (adiponectin receptor
XX splice variant) nucleic acid molecule. Adiponectin
XX (Acrp30/AdipoQ/apM1/GBP28) is the most abundant adipose-specific hormone
XX and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-
XX atherogenic adipokine. The polynucleotide of the invention demonstrates
XX antidiabetic, antibacterial, antiarteriosclerotic, cardiovascular-gen.,
XX cardiant, antiinflammatory, antilipemic, antibacterial, anorectic,
XX cytosolic, virucide, antithyroid, metabolic, anabolic and eating-
XX disorders-gen. activities. The polypeptides and their modulators may be
XX useful for preventing, treating or ameliorating a disorder selected from
XX metabolic disorders, inflammatory disorders, cardiovascular disorders,
XX obesity, diabetes, type II diabetes, type I diabetes, gestational
XX diabetes, early onset diabetes, insulin resistance, disorders in which
XX glucose-lowering would be beneficial, disorders in which amelioration of
XX insulin resistance would be beneficial, disorders in which suppressed FA
XX influx into liver would be beneficial, disorders in which reduced serum
XX TG would be beneficial, myocardial infarction, heart failure,
XX atherosclerosis, arteriosclerosis, disorders associated with aberrant
XX activity or expression of an adiponectin receptor, disorders associated
XX with aberrant vascular smooth muscle proliferation, disorders associated
XX with aberrant foam cell formation, disorders in which inhibition of
XX macrophage phagocytosis would be beneficial, disorders in which
XX inhibition of TNF-alpha production would be beneficial, dyslipidemia,
XX diabetic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,
XX hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The
XX polypeptides and polynucleotides can also be used in diagnosing,

CC preventing and treating cancer, and bacterial or viral infectious
CC disorders. The current sequence is that of a murine AdipoR (adiponectin
CC receptor) protein of the invention.
XX
XX Sequence 375 AA;
Query Match 97.3%; Score 1954; DB 9; Length 375;
Best Local Similarity 96.8%; Pred. No. 3.2e-208; Indels 0; Gaps 0;
Matches 363; Conservative 5; Mismatches 7;
QY 1 MSHKSGSVVAAQNGAPASNRREADTVLAEELGPLEEKGRVIANPPKAESEEQTCVPQEE 60
DB 1 MSHKSGSAGAQNGAPSGNRREADTVLAEELGPLEEKGRVIANPPKAESEEQTCVPQEE 60
QY 61 EBEVRVLTPLQAHAMERKESFVYKWEGRWRVPIYDVLVDWLKNDYLLHGHRRPMP 120
DB 61 EBEVRVLTPLQAHAMERKESFVYKWEGRWRVPIYDVLVDWLKNDYLLHGHRRPMP 120
QY 121 FRACFKSIPIRIHTETGNIWTHLLGFVLFPLGLTLMRPNMYFMAPLQEKVFGMEFLGA 180
DB 121 FRACFKSIPIRIHTETGNIWTHLLGFVLFPLGLTLMRPNMYFMAPLQEKVFGMEFLGA 180
QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFSCPPRLIYLS 240
DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFSCPPRLIYLS 240
QY 241 IVCVLGISAIIVQWDRPATPKHROTQTRAGVFLGLSLGVVPTMHTIAGFVKATTVGQM 300
DB 241 IVCVLGISAIIVQWDRPATPKHROTQTRAGVFLGLSLGVVPTMHTIAGFVKATTVGQM 300
QY 301 GWFFLMAVMYITGAGLYAARIPEPFPKFDIWFQSHOIFHVLVVAFAFVHFYGVSNLQE 360
DB 301 GWFFLMAVMYITGAGLYAARIPEPFPKFDIWFQSHOIFHVLVVAFAFVHFYGVSNLQE 360
QY 361 FRYGLEGGCTDITLL 375
DB 361 FRYGLEGGCTDITLL 375
RESULT 13
AAU30936
ID AAU30936 standard; protein; 387 AA.
XX
XX AAU30936;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #1427.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX W0200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSB-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX

PS	Claim 20; Page 379; 765pp; English.	
XX	The invention relates to novel human secreted polypeptides. The	
CC	polypeptides and antibodies to the polypeptides are useful for	
CC	determining the presence of or predisposition to a disease associated	
CC	with altered levels of polypeptide. The polypeptides are also useful for	
CC	identifying agents (agonists and antagonists) that bind to them. Cells	
CC	expressing the proteins are useful for identifying a therapeutic agent	
CC	for use in treatment of a pathology related to aberrant expression or	
CC	physiological interactions of the polypeptide. Vectors comprising the	
CC	nucleic acids encoding the polypeptides and cells genetically engineered	
CC	to express them are also useful for producing the proteins. The proteins	
CC	are useful in genetic vaccination, testing and therapy, and can be used	
CC	as nutritional supplements. They may be used to increase stem cell	
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon	
CC	and/or nerve tissue growth or regeneration; immune suppression and/or	
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.	
CC	AAU29510-AAU33304 represent the amino acid sequences of novel human	
CC	secreted proteins of the invention	
XX		
SQ	Sequence 387 AA;	
	Query Match 84.4%; Score 1696; DB 4; Length 387;	
	Best Local Similarity 89.1%; Pred. No. 1.8e-179;	
	Matches 335; Conservative 5; Mismatches 28; Indels 8; Gaps 8;	
QY	1 MSHKGSVVAQNGAPASNRADTVELAEGLPILLEKGRVIANPPKAEEOCTCPVQEE 60	
DB	11 MSHKGSVVAQNGAPASNRADTVELAEGLPILLEKGRVIANPPKAEEOCTCPVQEE 70	
QY	61 EEEVRVLTPLQAHAMEKNEEFVYKWEGRWVPIYDVLDPWLKNDYLLGHRPPMPS 120	
DB	71 EEEVRVLTPLQAHAMEKNEEFVYKWEGRWVPIYDVLDPWLKNDYLLGHRPPMPS 130	
QY	121 FRACPKSIFRIHTETGNITWHL-LGFVFLFLGLTLMRLPNMYFMAPLOE-KVFGWFFL 178	
DB	131 FRACPKSIFRIHTETGNITWHLALGFVFLFLGLTLMRLPNMYFMAPLOEKKVFGWFFL 190	
QY	179 GAVLCLSFSLWLFHTVYCHSEKYSRTFSKLD-YSGIALLTWSG-FVPLWLYSFCSPQRL 236	
DB	191 GAVLCLSFSLWLFHTAYCHFGVFPSTPQRELFKGLLLNMGELWSGLYSFCSPQRL 250	
QY	237 IYLSIVCVLGISAIIVQWDRFATPKHRTQAGVFLGLGLSGVVPMTHTTIA-EGFVKAT 295	
DB	251 IYLSIVCVLGISAIIVQWDRFATPKHRTQAGVFLGLGLSGVVPMTHTNRWALSAT 310	
QY	296 TVGQMGWFFLMAVYITG-AGLYAARIPERFPFGKFDIWFQSHQIPHVLVWAAAFVHYG 354	
DB	311 TVGQMGWFFLMAVYITGKLAFAARIPERFPFGKFDIWFQSHQIPHVLVWAAAFVHYG 370	
QY	355 -VSNLQEPFY-GLGG 368	
DB	371 SVSNLQEPFLTLEGG 386	
RESULT 14		
ID	ADW24251	
XX	ADW24251 standard; protein; 381 AA.	
AC	ADW24251;	
XX		
DT	24-MAR-2005 (first entry)	
XX		
DE	Human AdipoR3v1 (adiponectin receptor 3 splice variant 1) protein.	
XX		
KW	antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;	
KW	cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;	
KW	cytostatic; virucide; antithyroid; metabolic; anabolic;	
KW	eating-disorders-gen.; metabolic disorder; inflammation;	
KW	cardiovascular disease; nutritional disorder; obesity;	
KW	insulin dependent diabetes; non-insulin dependent diabetes;	
KW	insulin resistance; myocardial infarction; cardiac failure;	
KW	atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;	
KW	hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;	
KW	viral infection; AdipoR3v1; adiponectin receptor 3.	
XX	Homo sapiens.	
OS	WO2005001061-A2.	
FN	06-JAN-2005.	
PD		
XX	24-JUN-2004; 2004WO-US020399.	
PF		
XX	25-JUN-2003; 2003US-0482324P.	
PR	10-JUL-2003; 2003US-0486036P.	
PR	04-AUG-2003; 2003US-0492470P.	
PR	02-OCT-2003; 2003US-0508225P.	
PR	11-MAR-2004; 2004US-0552084P.	
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.	
PA		
XX	Chen J, Wu S, Lee N;	
PI		
XX	WPI: 2005-075549/08.	
DR	N-PSDB; ADW24250.	
DR		
XX	New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding	
PT	nucleic acid, useful for diagnosing, preventing and/or treating a	
PT	disorder related to aberrant adiponectin binding activity and/or	
PT	expression.	
XX	Claim 5; SEQ ID NO 102; 469pp; English.	
PS	The invention relates to a novel isolated AdipoRv (adiponectin receptor	
CC	splice variant) nucleic acid molecule. Adiponectin	
CC	(Acrp30/AdipoQ/apM1/GBP28) is the most abundant adipose-specific hormone	
CC	and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-	
CC	atherogenic adipokine. The polynucleotide of the invention demonstrates	
CC	antidiabetic, antibacterial, antiarteriosclerotic, cardiovascular-gen.,	
CC	cardiant, antiinflammatory, antilipemic, antibacterial, anorectic,	
CC	cytostatic, virucide, antithyroid, metabolic, anabolic, and eating-	
CC	disorders-gen. activities. The polypeptides and their modulators may be	
CC	useful for preventing, treating or ameliorating a disorder selected from	
CC	metabolic disorders, inflammatory disorders, cardiovascular disorders,	
CC	obesity, diabetes, type II diabetes, type II diabetes, gestational	
CC	diabetes, early onset diabetes, insulin resistance, disorders in which	
CC	glucose-lowering would be beneficial, disorders in which amelioration of	
CC	insulin resistance would be beneficial, disorders in which suppressed FA	
CC	influx into liver would be beneficial, disorders in which reduced serum	
CC	TG would be beneficial, myocardial infarction, heart failure,	
CC	atherosclerosis, arteriosclerosis, disorders associated with aberrant	
CC	activity or expression of an adiponectin receptor, disorders associated	
CC	with aberrant vascular smooth muscle proliferation, disorders associated	
CC	with aberrant foam cell formation, disorders in which inhibition of	
CC	macrophage phagocytosis would be beneficial, disorders in which	
CC	inhibition of TNF-alpha production would be beneficial, dyslipidemia,	
CC	diabetic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,	
CC	hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The	
CC	polypeptides and polynucleotides can also be used in diagnosing,	
CC	preventing and treating cancer, and bacterial or viral infectious	
CC	disorders. The current sequence is that of a human AdipoRv (adiponectin	
CC	receptor splice variant) protein of the invention.	
XX		
SQ	Sequence 381 AA;	
	Query Match 76.1%; Score 1529; DB 9; Length 381;	
	Best Local Similarity 79.9%; Pred. No. 7.2e-161;	
	Matches 306; Conservative 15; Mismatches 52; Indels 10; Gaps 4;	
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DB	1 MSHKGSVVAR-NGAPASNRRTDMVELAESELSPLQEKGWVITPNPKAEEOCTCPVQ 59	
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Db 60 EEEVWVLTPLQAHHTMKMEFVVKLTSCCH-HQVDGLPDWLKNDCLQNDCLLY 118
 QY 113 GHRPPSPFRACFKSIFRIHTETGNIWTHLLGFVLFGLTLMRPNNYFNAPLQKVV 172
 Db 119 GHRQWSSFWACFKSIFYIHTETGSSRTHLLGFVLFLEILTMLAPNNYFTAPLQEKVI 178
 QY 173 FGMFFLGAVLCFSWLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSPYCS 232
 Db 179 WRIFLLGAVLSFSWLVRTVYCHSEKVSRTFSKLDYSGIAPLLIRSFVPLWLYSPYCS 238
 QY 233 QPRLIYLSIVCVLIGISAIIVADREAPTKHROTTRAGVFLGLSGVPTMTHTIAEGFV 292
 Db 239 QPRLIYFSIYVIGISAIIVQDNRFTVPHROTTRAGVLLGLSGIVPTMTHTIAEGFV 298
 QY 293 KATTVQMGWFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHF 352
 Db 299 KATTVQMGWFFFLVAVMYITRAGLYAALIPERFPFGKLDIWFQSQIFHVLVTVAFVHF 358
 QY 353 YGVSNLOEFYRLEGCTDITLL 375
 Db 359 CGVSNLQEFHYSGREGCTDITLL 381

RESULT 15

ADR09023
 ID ADR09023 standard; protein; 386 AA.

AC ADR09023;

DT 04-NOV-2004 (first entry)

DE Human protein useful for treating neurological disease Seq 2529.

KW human; oligo-capping method; diagnostic marker; gene therapy;
 KW osteoporosis; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; dementia; short memory; cancer;
 KW sense or motor function; emotional reaction; fear response; panic;
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
 KW tranquiliser.

XX Homo sapiens.

XX EP1447413-A2.

XX 18-AUG-2004.

XX 12-FEB-2004; 2004EP-00003145.

XX 14-FEB-2003; 2003JP-00102207.

XX 09-MAY-2003; 2003JP-00131452.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;

XX WPI; 2004-583265/57.

XX N-PSDB; ADR07067.

XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 2529; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA
 CC molecules and the encoded proteins thereof. Specifically, it refers to
 CC cDNA clones obtained by an oligo-capping method, where none of these
 CC clones are identical to any known human mRNAs. The present invention
 CC describes an immunosay to identify agonists and antagonists, as well as
 CC antibodies, antisense molecules and siRNAs that can all be used to bind
 CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in

CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cyostatic and tranquiliser activities. This polypeptide is a protein
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This
 CC sequence is not given in the sequence listing of the specification but
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
 CC office.

XX Sequence 386 AA;

SQ Query Match 69.9%; Score 1403.5; DB 8; Length 386;

Best Local Similarity 70.7%; Pred. No. 78-147; Indels 7; Gaps 3;
 Matches 260; Conservative 43; Mismatches 58;

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Db 23 KGHQDGTGRGNDSDHQDLEFILEAS---VLSSHKKSSSEHEYSDEAPQDEGFMGMS 79

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Db 80 PL-LQAHAMEROMEFVYKVGWRVRVPHDVLDPWLKNDYLLHGRPPMPSFRACFKS 138

QY 128 IFRIHTETGNIWTHLLGFVLFGLTLMRPNNYFNAPLQKVVFGMFFLGAVLCFS 187

Db 139 IFRIHTETGNIWTHLLGCVFFLCGLGIFYMFRFNISFVAPLQEKVFGMFFLGAVLCFS 198

QY 188 WLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSPYCSPOPRIYLSIVCVLGI 247

Db 199 WLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSPYCSPOPRIYLSIVCVLGI 258

QY 248 SAIIVAQNDREAPTKHROTTRAGVFLGLSGVPTMTHTIAEGFVNAKTTVGQWPFLLMA 307

Db 259 AAIIVSQWDMFATPQYRGVAGVFLGLSGIIPTLHYVISBGLKAAITGIGLMLMA 318

QY 308 VMIITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEFYRLEG 367

Db 319 SLVITGAGLYAARIPERFPFGKDIWFHSHQLFHFVAVAGFVHFHGVSNLOEFYRLEMIG 378

QY 368 GCTDDITLL 375

Db 379 GCSEEDAL 386

Search completed: April 19, 2006, 13:57:15

Job time : 219.657 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
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 Run on: April 19, 2006, 14:18:45 ; Search time 127.967 Seconds
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 Total number of hits satisfying chosen parameters: 1867569
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
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 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
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 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	3	US-09-965-529-5
2	2009	100.0	375	3	US-09-969-680A-5
3	2009	100.0	375	4	US-10-264-237-2289
4	2009	100.0	375	5	US-10-799-943-2
5	2009	100.0	375	5	US-10-874-923-7
6	2009	100.0	375	6	US-11-048-692-5
7	1967	97.9	375	5	US-10-874-923-165
8	1954	97.3	375	5	US-10-799-943-6
9	1954	97.3	375	5	US-10-874-923-8
10	1529	76.1	381	5	US-10-874-923-102
11	1403.5	69.9	386	5	US-10-874-923-2
12	1391.5	69.3	386	5	US-10-874-923-4
13	1378.5	68.6	386	5	US-10-874-923-167
14	1378	68.6	311	5	US-10-799-943-8
15	1378	68.6	311	5	US-10-874-923-10
16	1376	68.5	421	5	US-10-874-923-104
17	1347	67.0	299	5	US-10-799-943-4
18	1345	66.9	299	5	US-10-874-923-9
19	1344	66.9	299	4	US-10-236-392-42
20	1075	53.5	201	3	US-09-948-783-131
21	1075	53.5	202	3	US-09-892-877-129
22	1052.5	52.4	288	5	US-10-874-923-6
23	1016.5	50.6	444	6	US-11-097-143-11043
24	1001.5	49.9	322	6	US-11-097-143-25536
25	674	33.5	228	4	US-10-264-237-2158
26	662	33.0	238	4	US-10-080-334-124
27	583	29.0	286	4	US-10-004-378A-134

28	501	24.9	360	4	US-10-424-599-252700	Sequence 252700,
29	499	24.8	384	4	US-10-425-114-51693	Sequence 51693, A
30	498.5	24.8	351	4	US-10-425-115-243901	Sequence 243901,
31	482.5	24.0	435	4	US-10-425-114-56352	Sequence 56352, A
32	482.5	24.0	438	4	US-10-425-114-73037	Sequence 73037, A
33	482	24.0	379	4	US-10-437-963-187447	Sequence 187447,
34	481	23.9	380	5	US-10-739-930-9197	Sequence 9197, Ap
35	477	23.7	345	5	US-10-739-930-7323	Sequence 7323, Ap
36	475.5	23.7	380	4	US-10-425-115-330861	Sequence 330861,
37	475	23.6	402	4	US-10-437-963-137004	Sequence 127004,
38	475	23.6	430	4	US-10-425-114-63314	Sequence 63314, A
39	475	23.5	440	4	US-10-739-930-8435	Sequence 8435, Ap
40	471.5	23.5	348	5	US-10-739-930-7324	Sequence 7324, Ap
41	471.5	23.5	380	5	US-10-437-963-159720	Sequence 159720,
42	465	23.1	376	4	US-10-437-963-182445	Sequence 182445,
43	461.5	23.0	370	4	US-10-483-512-32	Sequence 32, Appl
44	397.5	19.8	311	5	US-10-483-512-32	Sequence 32, Appl
45	372	18.5	210	4	US-10-424-599-178844	Sequence 178844,

ALIGNMENTS

RESULT 1

US-09-965-529-5
 ; Sequence 5, Application US/09965529
 ; Publication No. US20020182671A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: YUE, Henry
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil
 ; APPLICANT: AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariyah R.
 ; APPLICANT: LU, Dying Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731 USA
 ; CURRENT APPLICATION NUMBER: US/09/965,529
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
 ; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020182671A1 2071941CD1
 US-09-965-529-5
 Query Match 100.0%; Score 2009; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-182;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSHKGSVVAQNGAPASNRADTVLAEIPLLEKGRKRVIANPPKAEEOCTCPVPOEE 60
 Db 1 MSHKGSVVAQNGAPASNRADTVLAEIPLLEKGRKRVIANPPKAEEOCTCPVPOEE 60
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 Db 61 EEEVRVLTLPLOAHAMKMEEFVYKWEGRWVPIYDVLDPDLKNDYLLHGRHPMPS 120
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 Db 121 FRACFSIPIRIHTETGNITWHLGFLVFLPLGILTMLRPNMYMAPLOEKVFGMFLGA 180
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 Db 181 VLCLFSWLPHTYVCHSEKVSRTFSKLDYSGIALLMGSPVPMYYSFYCSPQRIIYLS 240


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; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/JP03/07515
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002-383738
; PRIOR FILING DATE: 2002-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-799-943-2

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Best Local Similarity 100.0%; Pred. No. 1.5e-182;
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DB 301 GWFFFLMVMYITGAGLYAARIPIERFPFGKEDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360

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RESULT 5
US-10-874-923-7
; Sequence 7, Application US/10874923
; Publication No. US2005032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-874-923-7

Query Match      100.0%; Score 2009; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKAESEOTCPVPOEE 60
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QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRNRVPIYDVLPDWLKNDYLLHGRPPMPS 120
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DB 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGLILTMLRPNMYFMAPLOEKVFGMFFLGA 180

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DB 241 IVCVLGISAIIVAOQDRFATPKHROTQTRAGVFLGLGLSGVVPVTHFTIABGFVKATTVGOM 300

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RESULT 5
US-10-874-923-7
; Sequence 7, Application US/10874923
; Publication No. US2005032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-874-923-7

Query Match      100.0%; Score 2009; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKAESEOTCPVPOEE 60
DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKAESEOTCPVPOEE 60

QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRNRVPIYDVLPDWLKNDYLLHGRPPMPS 120
DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRNRVPIYDVLPDWLKNDYLLHGRPPMPS 120

QY 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGLILTMLRPNMYFMAPLOEKVFGMFFLGA 180
DB 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGLILTMLRPNMYFMAPLOEKVFGMFFLGA 180

QY 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240
DB 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSFYCSQPRLIYLS 240

QY 241 IVCVLGISAIIVAOQDRFATPKHROTQTRAGVFLGLGLSGVVPVTHFTIABGFVKATTVGOM 300
DB 241 IVCVLGISAIIVAOQDRFATPKHROTQTRAGVFLGLGLSGVVPVTHFTIABGFVKATTVGOM 300

QY 301 GWFFFLMVMYITGAGLYAARIPIERFPFGKEDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
DB 301 GWFFFLMVMYITGAGLYAARIPIERFPFGKEDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360

QY 361 FRYGLEGGCTDDTL 375
DB 361 FRYGLEGGCTDDTL 375

RESULT 6
US-11-048-692-5
; Sequence 5, Application US/11048692
; Publication No. US20050123990A1
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: BURFORD, Neil; AZIMZAI, Valda
; APPLICANT: BAUGHN, Maria R.; LU, Dyoung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/11/048,692
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US/09/969,680
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2071941CD1
; US-11-048-692-5

Query Match      100.0%; Score 2009; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKAESEOTCPVPOEE 60
DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKAESEOTCPVPOEE 60
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Db      1  MSHKGSVVAQNGAPASNREADTVLAEGLPLEEKGKRVIANPPKABEEQTCVPQBE 60
Qy      61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Db      61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Qy     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
Db     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
Qy     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Db     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Qy     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Db     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Qy     361  FRYLEGCGCTDDTL 375
Db     361  FRYLEGCGCTDDTL 375

RESULT 7
US-10-874-923-165
; Sequence 165, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; PRIOR FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-874-923-165

Query Match      97.9%; Score 1967; DB 5; Length 375;
Best Local Similarity 97.6%; Pred. No. 1.5e-178;
Matches 366; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1  MSHKGSVVAQNGAPASNREADTVLAEGLPLEEKGKRVIANPPKABEEQTCVPQBE 60
Db      1  MSHKGSVVAQNGAPASNREADTVLAEGLPLEEKGKRAATSPAKABEEQACVPQBE 60
Qy     61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Db     61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Qy     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
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Db     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
Qy     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Db     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Qy     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Db     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Qy     361  FRYLEGCGCTDDTL 375
Db     361  FRYLEGCGCTDDSL 375

RESULT 8
US-10-799-943-6
; Sequence 6, Application US/10799943
; Publication No. US20040241802A1
; GENERAL INFORMATION:
; APPLICANT: KADOWAKI, Takashi
; APPLICANT: YAMAUCHI, Toshimasa
; APPLICANT: NAGAI, Ryozi
; APPLICANT: KAMON, Jyunji
; TITLE OF INVENTION: ADIPONECTIN RECEPTOR AND GENE ENCODING
; FILE REFERENCE: ARV-002
; CURRENT APPLICATION NUMBER: US/10/799,943
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/JF03/07515
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002-383738
; PRIOR FILING DATE: 2002-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-799-943-6

Query Match      97.3%; Score 1954; DB 5; Length 375;
Best Local Similarity 96.8%; Pred. No. 2.7e-177;
Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      1  MSHKGSVVAQNGAPASNREADTVLAEGLPLEEKGKRVIANPPKABEEQTCVPQBE 60
Db      1  MSHKGSAGAQNGAPSGNREADTVLAEGLPLEEKGKRAASSPAKABEEQACVPQBE 60
Qy     61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Db     61  EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVIPYDVLDPWLKNDYLLHGHRRPMP 120
Qy     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db     121  FRACFKSIFRIHTETGNIWTHLLGFVLFPLGLILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
Db     181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVYFVYCSQPRLIYLS 240
Qy     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Db     241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGQM 300
Qy     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Db     301  GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360
Qy     361  FRYLEGCGCTDDTL 375
Db     361  FRYLEGCGCTDDSL 375
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RESULT 9
US-10-874-923-8
; Sequence 8, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-874-923-8

Query Match          97.3%; Score 1954; DB 5; Length 375;
Best Local Similarity 96.8%; Pred. No. 2.7e-177;
Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 MSHKGSVVAQNGAPASNREADTVELAEGLPILLEKGGKRVIANPPKABEEQTCVPQOE 60
Db      1 MSHKGSAGAGQNGAPSGNREADTVELAEGLPILLEKGGKRAASPAKABEDQCPVQEE 60

QY      61 EEEVRVLTLPLOAHAMEKMEEFYKVGWRVRVPIYDVLDPDLKNDYLLHGRPPMP 120
Db      61 EEEVRVLTLPLOAHAMEKMEEFYKVGWRVRVPIYDVLDPDLKNDYLLHGRPPMP 120

QY      121 FRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFAPLOEKVFGMFLGA 180
Db      121 FRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFAPLOEKVFGMFLGA 180

QY      181 VLCLSPFWLFTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSPQRLIYLS 240
Db      181 VLCLSPFWLFTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSPQRLIYLS 240

QY      241 IVCVLGISALIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFVKATTYGM 300
Db      241 IVCVLGISALIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFVKATTYGM 300

QY      301 GWFFLMAVMYITAGLVAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
Db      301 GWFFLMAVMYITAGLVAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360

QY      361 FRYLEGCGCTDDTL 375
Db      361 FRYLEGCGCTDDSL 375

RESULT 10
US-10-874-923-102
; Sequence 102, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
```

```
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 102
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-874-923-102

Query Match          76.1%; Score 1529; DB 5; Length 381;
Best Local Similarity 79.9%; Pred. No. 8.8e-137;
Matches 306; Conservative 15; Mismatches 52; Indels 10; Gaps 4;

QY      1 MSHKGSVVAQNGAPASNREADTVELA--ELGPLLEKGGKRVIANPPKABEEQTCVPVQ 58
Db      1 MSHKGSVVAR-NGAPASNRETDVLEAESELSPLLQEKGWVITNPNKABEEQTCVPVQ 59

QY      59 EEEVRVLTLPLOAHAMEKMEEFYKVGWRVRVPIYDVLDPDLK-----DNDYLLH 112
Db      60 EEEVRVLTLPLOAHHTMEKMEEFYKLTQSCCH-HQYDGLDPLDKONDCLQDNDCLLY 118

QY      113 GHRPMPSPRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFAPLOEKVV 172
Db      119 GHRQMPSSFWACFKSIFYIHTETGSRTHLLGFVLFLFLGILTMLRPNMYFAPLOEKVI 178

QY      173 FGMFLGAVLCLSPFWLFTVYCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSP 232
Db      179 WRIFLGLAVLSLSPFWLFTVYCHSEKVSRTFSKLYSGIALLIRSFVPMLYSYFCSP 238

QY      233 QRLIYLSIVCVLGISALIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFV 292
Db      239 QRLIYFSIIYVVLGISALIVDQWDRFVTPKHQTRAGVLLGLGLSGIVPTMHPPIAEGFV 298

QY      293 KATTVGQMGFFLMAVMYITAGLVAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHF 352
Db      299 KATTVGQMGFFLVAVMYITRAGLYAALIPERFFPGKLDIWFQSQQIFHVLVTVAFVHF 358

QY      353 YGVSNLQEFYRGLGCGCTDDTL 375
Db      359 CGVSNLQEFYHSGEGCTDSSL 381

RESULT 11
US-10-874-923-2
; Sequence 2, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
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QY 243 CVLGISAIIVAOQDRFATPKHROTQAGVFLGLGLSGVVPMTMHFTIAEGFVKATTVQMGW 302
Db 254 CVLGIAAIIVSQMDMFATPQVRGAVFVGLGLSGIIPTHVVISSEGLKAATIRQIGW 313
QY 303 FFLMAVYITGAGLYAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEPR 362
Db 314 LMLMASLIYITGAALYAARIPIPERFFPGKDIWFHSHQLFHIFVVGAGFVHFHGVSNLOEPR 373
QY 363 YGLEGGCTDITLL 375
Db 374 FMIGGGCTEKDAL 386

RESULT 14
US-10-799-943-8
; Sequence 8, Application US/10799943
; Publication No. US20040241802A1
; GENERAL INFORMATION:
; APPLICANT: KADOWAKI, Takashi
; APPLICANT: YAMAUCHI, Toshimasa
; APPLICANT: NAGAI, Ryozo
; APPLICANT: KAWON, Jyunji
; TITLE OF INVENTION: ADIPONECTIN RECEPTOR AND GENE ENCODING
; FILE REFERENCE: ARV-002
; CURRENT APPLICATION NUMBER: US/10/799,943
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/JP03/07515
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002-383738
; PRIOR FILING DATE: 2002-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-799-943-8

Query Match 68.6%; Score 1378; DB 5; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.6e-122;
Matches 244; Conservative 31; Mismatches 30; Indels 0; Gaps 0;

QY 71 LQAHAMERKEEFVYKWEGRWRVIPYDVLPMKNDYLLHGRPPMPSPFRACFKSIFR 130
Db 7 LQAHAMERKEEFVCKWEGRWVIPHVDLPMLKNDYLLHGRPPMPSPFRACFKSIFR 66
QY 131 IHTETGNIWTHLLGFLVFLFLGILITMLRPNMYFMAPLQEKVFGMFFLGAVALCLSPSWLF 190
Db 67 IHTETGNIWTHLLGCVFFLCIGIFYMFRPNISFVAPLQEKVFGMFFLGAVALCLSPSWLF 126
QY 191 HTVYCHSEKVSRTSKLDYSGIALLIMSGFVPMLYSYFYCSQPRLIYLSIVCVLGISAI 250
Db 127 HTVYCHSEGVSRFLSKLDYSGIALLIMSGFVPMLYSYFYCNPCPFYILVIVICVLGIAAI 186
QY 251 IVAQWDRFATPKHROTQAGVFLGLGLSGVVPMTMHFTIAEGFVKATTVQMGWFFLMAVY 310
Db 187 IVSQWDMFATPQVRGAVFVGLGLSGIIPTHVVISSEGLKAATIRQIGWMLMASLY 246
QY 311 ITGAGLYAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEPRFYLEGGCT 370
Db 247 ITGAALYAARIPIPERFFPGKDIWFHSHQLFHIFVVGAGFVHFHGVSNLOEPRFMIGGCT 306
QY 371 DITLL 375
Db 307 EEDAL 311

RESULT 15
US-10-799-943-10
; Sequence 10, Application US/10874923
; Publication No. US20050032166A1

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; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-874-923-10

Query Match 68.6%; Score 1378; DB 5; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.6e-122;
Matches 244; Conservative 31; Mismatches 30; Indels 0; Gaps 0;

QY 71 LQAHAMERKEEFVYKWEGRWRVIPYDVLPMKNDYLLHGRPPMPSPFRACFKSIFR 130
Db 7 LQAHAMERKEEFVCKWEGRWVIPHVDLPMLKNDYLLHGRPPMPSPFRACFKSIFR 66
QY 131 IHTETGNIWTHLLGFLVFLFLGILITMLRPNMYFMAPLQEKVFGMFFLGAVALCLSPSWLF 190
Db 67 IHTETGNIWTHLLGCVFFLCIGIFYMFRPNISFVAPLQEKVFGMFFLGAVALCLSPSWLF 126
QY 191 HTVYCHSEKVSRTSKLDYSGIALLIMSGFVPMLYSYFYCSQPRLIYLSIVCVLGISAI 250
Db 127 HTVYCHSEGVSRFLSKLDYSGIALLIMSGFVPMLYSYFYCNPCPFYILVIVICVLGIAAI 186
QY 251 IVAQWDRFATPKHROTQAGVFLGLGLSGVVPMTMHFTIAEGFVKATTVQMGWFFLMAVY 310
Db 187 IVSQWDMFATPQVRGAVFVGLGLSGIIPTHVVISSEGLKAATIRQIGWMLMASLY 246
QY 311 ITGAGLYAARIPIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEPRFYLEGGCT 370
Db 247 ITGAALYAARIPIPERFFPGKDIWFHSHQLFHIFVVGAGFVHFHGVSNLOEPRFMIGGCT 306
QY 371 DITLL 375
Db 307 EEDAL 311

Search completed: April 19, 2006, 14:23:44
Job time : 128.967 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 19, 2006, 13:57:38 ; Search time 28.9318 Seconds
(without alignments)
1247.117 Million cell updates/sec

Title: US-10-799-943-2
 Perfect score: 2009
 Sequence: 1 MSSHKGSVVAQNGAPASNR.....SNLQEFYGLEGGCTDDTL 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs. 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : PIR_80:*
1:  _pir1:*
2:  _pir2:*
3:  _pir3:*
4:  _pir4:*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908	45.2	467	2 D88710	protein C43G2.1 [i
2	530.5	26.4	324	2 T39372	conserved hypothet
3	506.5	25.2	385	2 T04725	hypothetical prote
4	490.5	24.4	374	2 T05660	hypothetical prote
5	474	23.6	327	2 S61982	probable membrane
6	437	21.8	405	2 B85361	hypothetical prote
7	431.5	21.5	301	2 B84633	hypothetical prote
8	407	20.3	316	2 S69659	hypothetical prote
9	372	18.5	442	2 S62569	probable transmemb
10	251	12.5	543	2 S64850	probable membrane
11	173.5	8.6	93	2 H84832	hypothetical prote
12	168	8.4	108	2 T05657	hypothetical prote
13	151.5	7.5	205	2 E83042	conserved hypothet
14	149	7.4	219	2 S59367	hemolysin III - Ba
15	149	7.4	232	2 E97469	hypothetical 23.8K
16	149	7.4	232	2 A82688	Hemolysin III [imp
17	146.5	7.3	230	2 T29141	hypothetical prote
18	142.5	7.1	233	2 E70114	hemolysin III (ypl
19	137.5	6.8	210	2 AH1307	hemolysinIII prote
20	132.5	6.6	210	2 AH1679	hemolysinIII prote
21	132	6.6	211	2 H97016	probable membrane
22	132	6.6	215	2 A84008	hemolysin III BH28
23	129.5	6.4	238	2 D71250	probable hemolysin
24	127	6.3	219	2 H75342	probable hemolysin
25	125	6.2	217	2 A86687	hemolysin like pro
26	124.5	6.2	312	2 S51898	probable membrane
27	121.5	6.0	214	2 G97008	probable membrane
28	120.5	6.0	233	2 AF0110	probable hemolysin
29	116.5	5.8	215	2 C82372	probable hemolysin

30	114	5.7	218	2	AG3486	hemolysin III imp
31	114	5.7	411	2	F97760	hypothetical prote
32	112	5.6	215	2	G98036	conserved hypothet
33	112	5.6	215	2	G95170	hemolysin I impo
34	110.5	5.5	591	2	AG9231	transmembrane olig
35	110	5.5	393	1	C56274	ChrA homolog srpC,
36	109.5	5.5	219	2	AG0872	probable membrane
37	109.5	5.5	219	2	C91100	probable oxidoredu
38	109.5	5.5	219	2	C85074	probable oxidoredu
39	109.5	5.5	219	2	G85945	probable oxidoredu
40	108	5.4	213	2	D69938	hemolysin III homo
41	104.5	5.2	235	2	D19408	hypothetical prote
42	103	5.1	214	2	D28839	hemolysin III prot
43	102	5.1	254	2	E69853	conserved hypothet
44	102	5.1	716	2	AB1070	probable carbon st
45	102	5.1	721	2	A98293	probable carbon st

ALIGNMENTS

RESULT 1

ALB021 1
D88710
protein C43G2.1 [imported] - Caenorhabditis elegans

C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence revision 10-May-2001 #text change 31-Dec-2004

C;Accession: D88710
R:anonymous, The C. elegans Sequencing Consortium.
C;Date: 10-May-2001
C;Accession: Z04120

Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology and disease
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_el.
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2012-2018, 1998
A:Accession: D88710

Query Match	45.2%	Score	908;	DB	2;	Length	467;
Best Local Similarity	44.0%;	Pred.	No. 4.8e-66;				
Matches	175;	Conservative	60;	Mismatches	97;	Indels	66;
Gaps	6;						
Qy	3	SHKGSVVAQGNGAPASNREADTVLAEALGPLLEBKGRVIA-----	43				
Db	82	SRKTTVVSPNT---SDDEDADFCDSELLP--OQEGHRSRATSFAGRTAGSDDDEAMPGH	136				
Qy	44	-----NPPKA---EEBQTCPVPOEEEEVRVLPLPLQAHHAMEKN	80				
Db	137	TILYRRKKGGQWEINLOGTPDKRKDEBLEVDVKEDRSQTCIVT-----	184				
Qy	81	EETVYKVMEGRWRVIPDYDLDPWLKDNDYLHLGHRPMPSPRACFKSIPIRIHTGTNIWT	140				
Db	185	-----KTVEARKVKLYEHLPEWLDQNEFLRGHRPLPLPSSECFKSISWLSHTGTNIWT	239				
Qy	141	HLLGFVLFIFLGITLMURPNMYFWAPLOEKVVPFGMFFLGAVALCLSPMLFHTVYCHSEKV	200				
Db	240	HLIGCAVAFPFLLACWFLTRPDNHIO--FOEKVVVFSPFFAGAVLCGLSPFAFTLSCHSVNV	297				
Qy	201	SRTSKLDYSGIALLINGSFVPMLYSPYCSPQRLIYLSITCVLIGISAIIVAOMDRPAT	260				
Db	298	VKIFCKLDYMGISILLIGSFIPWHIYYGYCRREPKITIYAMWSVLGIGAIVSLMDKXSE	357				
Qy	261	PKHQTRAGVFLGLSGVWPTMTFTIAEGFKATTVGQMGMFFLMAVMYITGAGLYAAR	320				
Db	358	SRFPPIRAVFMGCSSVIETIHVIITDGVHSLPADNSFEHWLLMAFLYLIGAGLYATR	417				
Qy	321	IPERFFFPGKFIDWFQSHQIFHVLVVAAAFVHFVGSNL	358				

Db 418 TPERPPGKDIWFQSHQLFHTCVIAAFVHYGISEM 455

RESULT 2

conserved hypothetical protein SPBC12C2.09c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004

C:Accession: T39372

R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, September 1995

A:Reference number: Z21849

A:Accession: T39372

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-324 <DEV>

A:Cross-references: UNIPROT:Q09749; UNIPARC:UPI000013A262; EMBL:Z54140; PIDN:CAA90822.1;

A:Experimental source: strain 972h-; cosmid c12C2

C:Genetics:

A:Gene: SPDB-SPBC12C2.09c

A:Map position: 1

C:Superfamily: Adiponectin receptor protein and homologs

Query Match 26.4%; Score 530.5; DB 2; Length 324;

Best Local Similarity 39.8%; Pred. No. 1.4e-35;

Matches 107; Conservative 49; Mismatches 98; Indels 15; Gaps 4;

QY 94 VTPYDVLDPWLKNDYLLHGRPPMPSPFRACPKSIPRIHTETGNIWTHLLG---FVLPLF 150

DB 48 LLTDQLEPQQDQNIYISGVYPPSPFYLVCVKSIFVHNESVNIWTHLFGAIVLFFTF 107

QY 151 LGILTLRPNMFMAPLOEKVYVGMFPLGAVLCLSFWLFTVYCHSEKVSRTFSKLDYS 210

DB 108 KSELILKRTD---TTAEVDVYITVFLFSFAFTMLGCTPYHTISNHSDDVSFGNKLDTL 163

QY 211 GIALIMGSFVPLWLYSYFCSPQRLIYLSIVCVLGSIAIIVAQWDRFATPKHROTQAGV 270

DB 164 GIVMIVGSFICLVAFACHANFRTLYIGTIIGIVIVASTCLLDRFPQPMRPYRALI 223

QY 271 FLGLGLSGVVPVTH-----FTIAGFVKATTVGQMGFFLMVMVYITGAGLYAARIPERFF 326

DB 224 FVLMLGLFGIFPVITHALKISFSEILVRMLGV---WLLQGLFIYVGAIVIYALRIPEKWS 279

QY 327 RCKFDIWFQSHQIEHLVVAFAFVHYGV 355

DB 280 PGKYDVFSSQHFVHCVIIAFAFCHPHGV 308

RESULT 3

T04725

hypothetical protein F19F18.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004

C:Accession: T04725

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15382

A:Accession: T04725

A:Molecule type: DNA

A:Residues: 1-385 <BEV>

A:Cross-references: UNIPROT:Q9SZG0; UNIPARC:UPI00000A346B; EMBL:AL035605

A:Experimental source: cultivar Columbia; BAC clone F19F18

C:Genetics:

A:Map position: 4

A:Introns: 84/2; 168/3

A:Note: F19F18.170

C:Superfamily: Adiponectin receptor protein and homologs

Query Match 25.2%; Score 506.5; DB 2; Length 385;

Best Local Similarity 32.4%; Pred. No. 1.6e-33;

Matches 120; Conservative 57; Mismatches 114; Indels 79; Gaps 6;

QY 60 EBEVRVLTLPQAHAMEKEEFVYK-VWEG-RMRVIPDYDVLDPWLKNDYLLHGRPP 117

Db 3 DEAEIKHLKPOASSETMDKKHNVKGRKLVQKVKYQLVEFHSLPAYLRDNEVIIGHYRSE 62

QY 118 MPSFRACPKSIPRIHTETGNIWTHLLGFLVFLFLGILTMLR-PNMYFMAPLOEKV----- 171

Db 63 WP-IKQILLSTFTTHNETLNWTHLIGFPLFALTIYATKVPFVVDLHSLQHRLPDLLR 121

QY 172 ----- 171

Db 122 KTDLHLKLSLSELMARLPSSPSSWHVMDLLYNCLIPERFSGHNYTDMCVLHVSREDLANLIAP 181

QY 172 -----VFGMPFLGAVLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVP 222

Db 182 LIFRPITRWPFVAFGLGAMFCLLASSTCHLLSCHSERVSYIMLRDYAGIAALIAITSFYP 241

QY 223 WLYTSFYCSQPQRLIYLSIVCVLGSIAIIVAQWDRFATPKHROTQAGVFLGLGSLGVWPT 282

Db 242 PVIYSFMCDFPFCNLYLGFITILGIATVLSVLLPVFQSPFEPFVRVTRASLFFGFGFSGGLAPI 301

QY 283 MHFTIAGFVKATTVGQMGFFLMVMVYITGAGLYAARIPERFFPGKFDIWFQSHQIFHV 342

Db 302 LKLLII-FWDQPEALHTTGYILMGLLYGLGALVYATRIPERMWPGKFDIAGHSHQLFHV 360

QY 343 LVVAAAFVHF 352

Db 361 LVVAGAFTHY 370

RESULT 4

T05660

hypothetical protein F22113.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004

C:Accession: T05660

R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420

A:Accession: T05660

A:Molecule type: DNA

A:Residues: 1-374 <BEV>

A:Cross-references: UNIPROT:Q9SVF3; UNIPARC:UPI00000A1906; EMBL:AL035539

A:Experimental source: cultivar Columbia; BAC clone F22113

C:Genetics:

A:Map position: 4

A:Introns: 84/2; 168/3

A:Note: F22113.90

C:Superfamily: Adiponectin receptor protein and homologs

Query Match 24.4%; Score 490.5; DB 2; Length 374;

Best Local Similarity 31.6%; Pred. No. 3e-32;

Matches 117; Conservative 58; Mismatches 116; Indels 79; Gaps 6;

QY 60 EBEVRVLTLPQAHAMEKEEFVYK-VWEG-RMRVIPDYDVLDPWLKNDYLLHGRPP 117

Db 3 DEAEIKHLKPOASSETMDKKHNVKGRKLVQKVKYQLVEFHSLPAYLRDNEVIIGHYRSE 62

QY 118 MPSFRACPKSIPRIHTETGNIWTHLLGFLVFLFLGILTMLR-PNMYFMAPLOEKV----- 171

Db 63 WP-IKQILLSTFTTHNETLNWTHLIGFPLFALTIYATKVPFVVDLHSLQHRLPDLLR 121

QY 172 ----- 171

Db 122 KTDLHLKLSLSELMARLPSSPSSWHVMDLLYNCLIPERFSGHNYTDMCVLHVSREDLANLIAP 181

QY 172 -----VFGMPFLGAVLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVP 222

Db 182 LIFRPITRWPFVAFGLGAMFCLLASSTCHLLSCHSERVSYIMLRDYAGIAALIAITSFYP 241

QY 223 WLYTSFYCSQPQRLIYLSIVCVLGSIAIIVAQWDRFATPKHROTQAGVFLGLGSLGVWPT 282

Db 242 PVIYSFMCDFPFCNLYLGFITILGIATVLSVLLPVFQSPFEPFVRVTRASLFFGFGFSGGLAPI 301

QY 283 MHFTIAGFVKATTVGQMGFFLMVMVYITGAGLYAARIPERFFPGKFDIWFQSHQIFHV 342

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Db 302 LHKLIIT-FWDQPEALMTGYEILMGLYLGLGAVVYATRIPEWRMPGKFDIAGHSHQLFHV 360
QY 343 LVVAAAFVHF 352
Db 361 LVVAGALTHY 370

RESULT 5
S61982
probable membrane protein YOL002c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O2501; hypothetical protein UND327
C:Species: Saccharomyces cerevisiae
C:Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 31-Dec-2004
C:Accession: S61982; S66683; S72131
R:Starky, F.; Uhlen, M.
submitted to the EMBL Data Library, December 1995
A:Reference number: S61981
A:Accession: S61982
A:Molecule type: DNA
A:Residues: 1-327 <STE>
A:Cross-references: UNIPROT:Q12442; UNIPARC:UPI000006AC11; EMBL:U43491; NID:g1150992; P1
R:Pettersson, B.; Starky, F.; Uhlen, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66682
A:Accession: S66683
A:Molecule type: DNA
A:Residues: 1-327 <PET>
A:Cross-references: UNIPARC:UPI000006AC11; EMBL:Z74744; NID:g1419762; PIDN:CNA99001.1; F
A:Experimental source: strain S288C
R:Starky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacchar
A:Reference number: S72130; MUID:97051599; PMID:8896276
A:Accession: S72131
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-327 <STW>
A:Cross-references: UNIPARC:UPI000006AC11; EMBL:U43491; NID:g1150992; PIDN:AAC49478.1; F
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C:Genetics:
A:Cross-references: SGD:S0005362
A:Note: YOL002c
A:Superfamily: Adiponectin receptor protein and homologs
C:Keywords: transmembrane protein
F:93-109/Domain: transmembrane #status predicted <TM1>
F:126-142/Domain: transmembrane #status predicted <TM2>
F:164-180/Domain: transmembrane #status predicted <TM3>
F:191-207/Domain: transmembrane #status predicted <TM4>
F:225-241/Domain: transmembrane #status predicted <TM5>
F:255-271/Domain: transmembrane #status predicted <TM6>
F:294-310/Domain: transmembrane #status predicted <TM7>

Query Match 23.6%; Score 474; DB 2; Length 327;
Best Local Similarity 38.4%; Pred. No. 5.6e-31;
Matches 104; Conservative 45; Mismatches 116; Indels 6; Gaps 2;

QY 93 RVIPYDVLDPWLKNDYLLHGRHPMPSPRACFKSIPRIHTETGNIWTHL---LGFVLFL 149
Db 48 RLYSWDEIPWQRNDPILHGYVYKETSSTFETPKSLFYLHNSVNIYSHLIPALGFPTVL 107

QY 150 FLGILMTLRPNMYFMAPLQEKVVGFFLGLAVLCLSFSLFHTVYCHSEKVSRTESKLDY 209
Db 108 LLDKSTI---KVFATTTWLDHMDIFYSYGAFLILSSSFCLKSHSLRIATLGNKLDY 164

QY 210 SGILLIMSGFVFWLYYFSCSPQPLIYLSIVCVLGISAIIVQWDRPATPKHROTFRAG 269
Db 165 LGICILIVTSWVILYGYEKEKSLFCLFALITVSTGIACSIYSLKDKPKRWRPVRAG 224

QY 270 VFLGLGLSGVVPTMHTFIAGSGFKVATTVGQMGFFLMAVMYITGAGLYAARIPERFPFGK 329
Db 225 LFVCFGLSSIPIFSGLYCYFSFSIWTQIQLFWLLGGVLYIIGAVLYGNRPPEKICPGK 284

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QY 330 FDIWFQSHQIFHVLVVAFAAFVHFYGVSNLQE 360
Db 285 FDIWGHSHQLFHFVLVVAALCHLRGLNSYE 315

RESULT 6
B85361
hypothetical protein AT4G30850 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: B85361
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85361
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:O65564; UNIPARC:UPI00000A9BDD; GB:NC_001268; NID:g7269986; F
C:Genetics:
A:Gene: AT4G30850
A:Map position: 4
C:Superfamily: Adiponectin receptor protein and homologs

Query Match 21.8%; Score 437; DB 2; Length 405;
Best Local Similarity 35.1%; Pred. No. 7.2e-28;
Matches 106; Conservative 42; Mismatches 118; Indels 36; Gaps 5;

QY 93 RVIPYDVLDPWLKNDYLLHGRHPMPSPRACFKSIPRIHTETGNIWTHLGLFVLF--- 148
Db 30 RLMKFEELPRYLKDNF-IHNHYRCWSEIKETFLSAFWMHNETLNLTWHLCLGFAIPTWMM 88
QY 149 -----LFLGLTLMRPNNYFMAPLQEKVVFMPFGLAV 181
Db 89 VVSMETTELGLAGFVLLSGKIKQISIFLGLDLWLMTLWTEQQAGHGRQWCKQMFSPAI 148

QY 182 -LCLSFSLFHTVYCHSEKVSRTFKSLDYSGILLIMSGFVFWLYYFSCSPQPLIYLS 240
Db 149 KLCITS--MSHLFACHSRRLFFWRLDYAGISLMIVCSFFAPIIYAFSHTYWRFLYLS 206

QY 241 IVCVLGISAIIVQWDRPATPKHROTFRAGVFLGLSLGVVPTMHTFIAGSGFKVATTVGQM 300
Db 207 SISILGLLAIFTLSPSLSAPRFRSFRALFLTMGFSGVIPATHVLYLHKHNPVLLIA-L 265

QY 301 GWFFFLMAVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAFAAFVHFYGVSNLQE 360
Db 266 VTELAMAVDIATGAAPFYVTRIPERWRPGAFDIAGHSHQIFHVFVVLGALAHVASLLIND 325

QY 361 FR 362
Db 326 FR 327

RESULT 7
B84633
hypothetical protein At2g24150 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: B84633
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <STO>
A:Cross-references: UNIPROT:Q9ZUH8; UNIPARC:UPI00001788DA; GB:AE002093; NID:g4115375; P
C:Genetics:

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A:Gene: At2g24150
A:Map position: 2
C:Superfamily: Ad:

Query Match	21.5%	Score 431.5;	DB 2;	Length 301;
Best Local Similarity	35.7%	pred. NO. 1.5e-27;		
Matches 101;	Conservative	46;	Mismatches 91;	Indels 45;
	Gaps			

RESULT 8

Z0001
 S6959
 hypothetical protein YDR492w - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 31-Dec-2004
 C/Accession: S69659; S69664
 R/Dietrich, F. S.
 submitted to the EMBL Data Library, August 1995
 A/Description: The sequence of *S. cerevisiae* cosmids 9410, 8035, 8166, and 9787.
 A/Reference number: S69554

Query Match	20.3%	Score 407;	DB 2;	Length 316;
Best Local Similarity	35.8%	Pred. No. 1.5e-25;		
Matches 97;	Conservative 43;	Mismatches 109;	Indels 22;	Gaps 5;

RESULT 9

A:Accession: T38588
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-442 <PE2>
 A:Cross-references: UNIPROT:Q09910; UNIPARC:UPI0000013A0ED; EMBL:Z67961; NID
 A:Experimental source: strain 972h; cosmid c30D11
 C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
 C:Species: Schizosaccharomyces pombe
 C:Probable transmembrane protein - fission yeast (Schizosaccharomyces pombe)
 R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z21801
 A:Accession: T38588
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-442 <PE2>
 A:Cross-references: UNIPROT:Q09910; UNIPARC:UPI0000013A0ED; EMBL:Z67961; NID
 A:Experimental source: strain 972h; cosmid c30D11

Query Match 18.5%; Score 372; DB 2; Length 442;
Best Local Similarity 31.3%; Pred. No. 1.5e-22;
Matches 101; Conservative 48; Mismatches 136; Indels 38; Gaps 9

RESULT 10

PROBABLE MEMBRANE PROTEIN YLR023C - YEAST (*SACCHAROMYCES CEREVISIAE*)
 N; ALTERNATE NAMES: HYPOTHETICAL PROTEIN L1726
 C; SPECIES: *SACCHAROMYCES CEREVISIAE*
 C; DATE: 01-AUG-1995 #SEQUENCE_REVISION 24-MAY-1996 #TEXT_CHANGE 09-JUL-2004
 C; ACCESSION: S64850
 R; OBERMAIER, B.; PIRAVANDI, E.; RINKE, M.
 SUBMITTED TO THE PROTEIN SEQUENCE DATABASE, MAY 1996
 A; REFERENCE NUMBER: S64845
 A; ACCESSION: S64850
 A; MOLECULE TYPE: DNA
 A; RESIDUES: 1-543 <OBE>
 A; CROSS-REFERENCES: UNIPROT:Q007959; UNIPARC:UPI0000006A56D; ENMBL:Z73195; NID
 A; EXPERIMENTAL SOURCE: STRAIN S288C

F:431-447/Domain: transmembrane #status predicted <TW5>

Query Match 12.5%; Score 251; DB 2; Length 543;
 Best Local Similarity 24.0%; Pred. No. 1.3e-12;
 Matches 80; Conservative 48; Mismatches 132; Indels 74; Gaps 9;
 QY 90 GRWRVTPYDVLPMKNDYLLHGRPPMPSPACPKSIFRI-----HTETGNIWTHLL 143
 DB 211 GETQHLHYQLPFPFRENRYIIHGYR----FYNTSHKSLISIFNMYGWNETSNIWSHLL 266
 QY 144 GFVFLPLGLITLWLRPNMY--FWAPLQEKVVGFMEFLGAVLCSPGLPHTVYCHS-EKV 200
 DB 267 GAIYIYLAIDYPPQSEWNRNSOVPPQARWIVFMEFLAAKCMKLSVFWHTFNGTSFLKL 326
 QY 201 SRTFSKLDYSGIALLMGSPVPLWYSFYSCSPQRIYLSIVCLGISAIIVQAQMDRFAT 260
 DB 327 RSFKACVDYSGITILITASLTITTEFTVMYSCYWMYTIMSISLALGVFGVFNWNSRPRD 386
 QY 261 PKHROTQAGVFLGLGSGVVPVTHFTIAGFVKATTVGQWGP-----FLMAVMYITGAGL 316
 DB 387 PEARPLRIRPFILLATMGVLSPLHLIFLTDLHYAATL-----PSPVTYKSVVMYLVGVVF 441
 QY 317 YAARIPERF-----FPGKFDI----- 332
 DB 442 YGSFIPERFRSDVQDKTPTNYELSTDLIITKQREIHFPREVPTAHSKSCSPSHAKSF 501
 QY 333 ----WFO----SHQIFHLVVAFAAFVHFVGSNL 358
 DB 502 KSLWWDYFCCSTHFWFFVLGVIGHYRAILDM 535

RESULT 11

H84832
 Hypothetical protein At2g40710 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
 C:Accession: H84832
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: H84832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <STO>
 A:Cross-references: UNIPROT:Q7XJN5; UNIPARC:UPI00001623F9; GB:AE002093; NID:g4895222; PI
 C:Genetics:
 A:Gene: At2g40710
 A:Map position: 2
 C:Superfamily: Adiponectin receptor protein and homologs

Query Match 8.6%; Score 173.5; DB 2; Length 93;
 Best Local Similarity 47.6%; Pred. No. 3.5e-07;
 Matches 39; Conservative 12; Mismatches 24; Indels 7; Gaps 2;

QY 274 LGLSGVVPTWHFTIA-----EGFVKATTVGQWGFPLMAVMYITGAGLYAARIPERFPKGF 330
 DB 1 MGFSGLAPILHKLIFWDQPEALHTTCYBI-----LMGLLYGLGALVYATRIPIRPMWPKF 56
 QY 331 DIMFQSHQIFHLVVAFAAFVHF 352
 DB 57 DIAGHSHQLFHLVVAAGAFTHY 78

RESULT 12

T05657
 Hypothetical protein F22113.60 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C:Accession: T05657
 R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.H.

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420
 A:Accession: T05657
 A:Molecule type: DNA
 A:Residues: 1-108 <BEV>
 A:Cross-references: UNIPROT:Q9SVF6; UNIPARC:UPI00000A86C0; EMBL:AL035539
 A:Experimental source: cultivar Columbia; BAC clone F22113
 C:Genetics:
 A:Map position: 4
 A:Introns: 3/3; 42/1
 A:Note: F22113.60
 C:Superfamily: Adiponectin receptor protein and homologs

Query Match 8.4%; Score 168; DB 2; Length 108;
 Best Local Similarity 45.3%; Pred. No. 1.1e-06;
 Matches 39; Conservative 10; Mismatches 31; Indels 6; Gaps 1;

QY 273 GIGLSGVVPTWHFTIAGFVKATTVGO-----MGFFFLMAVMYITGAGLYAARIPERFP 326
 DB 8 GCGERAVSNEARSIQDIIIVAVIVTRREDIYLTGTEILMGLLYGLGALVYATRIPIRWM 67
 QY 327 PGKFDIWFQSHQIFHLVVAFAAFVHF 352
 DB 68 PGKFDIAGHSHQLFHLVVAAGAFTHY 93

RESULT 13

E83042
 conserved hypothetical protein PA4833 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2004
 C:Accession: E83042
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: E83042
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <STO>
 A:Cross-references: UNIPROT:Q9HUX7; UNIPARC:UPI00000C5E2E; GB:AE004896; GB:AE004091; NI
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4833
 C:Superfamily: hemolysin III

Query Match 7.5%; Score 151.5; DB 2; Length 205;
 Best Local Similarity 24.6%; Pred. No. 5.1e-05;
 Matches 62; Conservative 36; Mismatches 87; Indels 67; Gaps 11;

QY 132 HTETGNIWTHLLGFLV----FLPLGLITLWLRPNMYFMAPLQEKV-FGMFFLGAFLCLSP 186
 DB 3 HGERLNAWTHLLGAVAACTGAVLTVQASLNGSPW-----XIVGVGVYVTLTLLYSI 55
 QY 187 SMLFHTVYCHSKSVKSRFTSKLDYSGIALLMGSPVPLWYSFYSCSPQRIYLSIVCLVG 246
 DB 56 STAYSHVRCRAKVMR---KLDHLISYLLIAGSYTP-----PC-----LVTLRG 96
 QY 247 ISAIIVQAQDRPATPKHROTQAGVFLGLSGVVPVTHFTIAGFVKATTVGQWGFPLM 306
 DB 97 -----PMG-----WTLFGIVMGLAVLQMKIPRSEARVLSSVVVIYAVMGWIVLI 141
 QY 307 AVMYI-----TGAGLYAARIPERFPKGFDIWFQSHQIFHLVVAFAAFVHFY 353
 DB 142 AVKPLLAALGSAGFTWLAAGGVLYTVGVYAYDHRFRW---HGIWHLFVIAGSLILHFV 198
 QY 354 GVSNLQEPFRYGL 365
 DB 199 AI-----WRYVL 205

RESULT 14

S59967
hemolysin III - Bacillus cereus
N;Alternate names: hemolytic factor
C;Species: Bacillus cereus
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 31-Dec-2004
C;Accession: S59967; S52296
R;Baiba, G.B.; Kuzmin, N.P.
Biochim. Biophys. Acta 1264, 151-154, 1995
A;Title: Cloning and primary structure of a new hemolysin gene from Bacillus cereus.
A;Reference number: S59967; MUID:96085115; PMID:7495855
A;Accession: S59967
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <BAI>
A;Cross-references: UNIPROT:P54176; UNIPARC:UPI000012C94B; EMBL:X84058; NID:G662879; PID
C;Superfamily: hemolysin III

Query Match 7.4%; Score 149; DB 2; Length 219;

Best Local Similarity 24.3%; Pred. No. 8.8e-05;
Matches 59; Conservative 47; Mismatches 75; Indels 62; Gaps 13;

QY 131 IHTETGNITWHLGFLVFLGLTLMRLPNMYPMAPLQKVFQMGFFLGAIVCLSPSWLIF 190

DB 12 VKEEIANATHGIGAILSPALIIIIHASKHGTA--SAVVAFTVYGVSMFLLYLFSFTLL 69

QY 191 HTVYCHSEKVSRTFSKLDYSGIALLINGSFVPHLYSPYCSPQRLIYLSIVCVLGISAI 250

DB 70 HSI--HHPKVEKLFITLDHSAIYLLIAGTYTPEL-----LITLRGPLG---- 110

QY 251 IVAQMDRFATPKHQTRAGVFLGLSGVVPTMHFTIABGVKATTVGQ--MGWFFLMAV 308

DB 111 -----W-----TLALIIWTLAIGGIIFKIFF--VRRFIKASTLCYIIINGWLIIVAI 154

QY 309 --MY--ITGAG-----LYAARIPERFFPGKFDIWFQ---SHQIFHVLVVAFAFVHP 352

DB 155 KPLYENLTGHGFLSLLAGGLYS--VGAIFP-----LWEKLPFNHAIWHLFVLGGSAMMF 207

QY 353 YGV 355

DB 208 FCV 210

RESULT 15

E97469
hypotheical 23.8K protein in fldb-bgla intergenic region [imported] - Agrobacterium tum
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004
C;Accession: E97469
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E97469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <KUR>
A;Cross-references: UNIPROT:Q8UGX9; UNIPARC:UPI00000D198A; GB:AE007869; PIDN:AAK86710.1;
C;Genetics:
A;Gene: AGR C 1653
A;Map position: circular chromosome
C;Superfamily: hemolysin III

Query Match 7.4%; Score 149; DB 2; Length 232;

Best Local Similarity 25.0%; Pred. No. 9.4e-05;
Matches 56; Conservative 47; Mismatches 77; Indels 44; Gaps 13;

QY 141 HLLGFLVFLFLGLTLMRLPNMYFMA--PLQEKVVFQMGFFLGAIVCLSPSWLFTHTVYCHSE 198

DB 33 HGVG-IVFALIGATALI---FYAMAWGSLSAIAAAWIYGLGLVACLSVSTFTN-IWPHS- 86

QY 199 KVSRTFSKLDYSGIALLINGSFVPHLYSPFY---CSPQRLIYLSIVCVLGISAIIVAQW 255

Db 87 RVKWFRLRLDHSATPILIAATYTPFLMRGIHDPLIAVNLGLIWLAAICGILLKCLPGRY 146
QY 256 DRFATPKHQTRAGVFLGLSGVVPTMHFTIABGVKATTVGQMGFFLMAVVIITGAG 315
Db 147 DRVA-----IGLYLAWGWSGI---MVVPEPLSHLAPVTL-----W-----LIVAGGV 185
QY 316 LYAARIPERFFPGKFDIW----FQSHQIFHVLVVAFAFVHPYGV 355
Db 186 IYSLGV-----IPHWWEKLRFO-NAIWHGFFVVSAAAHHYFAV 221

Search completed: April 19, 2006, 14:03:23

Job time : 30.9318 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 19, 2006, 13:50:46 ; Search time 170.252 seconds
(without alignments)
1554.007 Million cell updates/sec

Title: US-10-799-943-2

Perfect score: 2009

Sequence: 1 MSHKGVVVAQNGAPASNR.....SNLQEFYRLEGCTDDTL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_tramb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	1 ADRL1_HUMAN	Q96a54 homo sapien
2	2009	100.0	375	2 Q53YV6_HUMAN	Q53YV6 homo sapien
3	2006	99.9	375	2 Q53HS7_HUMAN	Q53HS7 homo sapien
4	1967	97.9	375	2 Q6P746_RAT	Q6P746 rattus norv
5	1957	97.4	375	2 Q5V915_PIG	Q5V915 sus scrofa
6	1954	97.3	375	1 ADRL1_MOUSE	Q91vh1 mus musculu
7	1954	97.3	375	2 Q53YV4_MOUSE	Q53YV4 mus musculu
8	1842	91.7	348	2 Q6S015_PIG	Q6sq15 sus scrofa
9	1817	90.4	375	2 Q4PKP2_CHICK	Q4pkp2 gallus gall
10	1745	86.9	384	2 Q50100_XENLA	Q501q0 xenopus lae
11	1742	86.7	379	2 Q66KJ1_XENTR	Q66kj1 xenopus tro
12	1727	86.0	381	2 Q7ZY04_XENLA	Q7zy04 xenopus lae
13	1604.5	79.9	377	2 Q80300_BRARE	Q803q0 brachydanio
14	1573	78.3	318	2 Q4SS53_TETNG	Q4ss53 tetraodon n
15	1403.5	69.9	385	2 Q66K55_XENLA	Q66k55 xenopus lae
16	1403.5	69.9	386	1 ADRL2_HUMAN	Q86v24 homo sapien
17	1403.5	69.9	386	2 Q33YV5_HUMAN	Q33YV5 homo sapien
18	1398.5	69.6	386	2 Q5TYU5_BRARE	Q5tyu5 brachydanio
19	1397.5	69.6	386	2 Q5UVJ1_PIG	Q5uvj1 sus scrofa
20	1395.5	69.5	387	2 Q68ET2_XENLA	Q68et2 xenopus lae
21	1391.5	69.3	386	1 ADRL2_MOUSE	Q8bq5 mus musculu
22	1391.5	69.3	386	2 Q53YV3_MOUSE	Q53YV3 mus musculu
23	1387.5	69.1	364	2 Q4RH94_TETNG	Q4rh94 tetraodon n
24	1384.5	68.9	386	2 Q5ZMH3_CHICK	Q5zmh3 gallus gall
25	1372.5	68.3	386	2 Q4PKP1_CHICK	Q4pkp1 gallus gall
26	1083	53.9	206	2 Q5M1A8_PIG	Q5mia8 sus scrofa
27	1016.5	50.6	444	1 ADRL1_DROME	Q9vcv8 drosophila
28	971.5	48.4	324	2 Q7PQ98_ANOGA	Q7pq98 anopheles g
29	940	46.8	217	2 Q6SQ14_PIG	Q6sq14 sus scrofa
30	908	45.2	434	1 ADRL1_CABEL	Q94177 caenorhabdi
31	898	44.7	433	2 Q61U91_CABER	Q61u91 caenorhabdi

32	876	43.6	586	2	Q61UT2_CABER	Q61ut2 caenorhabdi
33	873.5	43.5	581	2	Q9N536_CABEL	Q9n536 caenorhabdi
34	761	37.9	395	2	Q5DGS4_SCHJA	Q5dgs4 schistosoma
35	632	31.5	117	2	Q512P6_PIG	Q512p6 sus scrofa
36	603	30.0	114	2	Q6T5C5_BOVIN	Q6t5c5 bos taurus
37	595	29.6	318	2	Q5B3E8_EMENI	Q5b3e8 aspergillus
38	589	28.3	321	2	Q521M8_MAGGR	Q521m8 magnaporthe
39	573	28.5	321	2	Q4WXS9_ASFFU	Q4wxs9 aspergillus
40	560	27.9	139	2	Q6T5C4_BOVIN	Q6t5c4 bos taurus
41	530.5	26.4	324	1	ADRL1_SCHPO	Q09749 schizosacch
42	515	25.6	315	2	Q7S0E1_NEUCR	Q7s0e1 neurospora
43	506.5	25.2	385	2	Q9SZG0_ARATH	Q9szg0 arabidopsis
44	491.5	24.5	374	2	Q67ZB8_ARATH	Q67zb8 arabidopsis
45	491	24.4	624	2	Q4PDS6_USTMA	Q4pds6 ustilago ma

ALIGNMENTS

RESULT 1
ID ADRL1_HUMAN STANDARD; PRT; 375 AA.
AC Q96A54; Q9Y360;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Adiponectin receptor protein 1 (Progestin and adipoo receptor family member I).
GN Name=ADIPOR1; Synonyms=PAQR1; ORFNames=CGI-45;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;
RA Lai C.-H., Chou C.-Y., Chang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Lung, and Skin;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klaunig R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Osofsky J.S., Abramson R.D., Mullaly S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.C., Krzywicki M.I., Skalek U., Smalish D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
TISSUE=SUBUNIT, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP MEDLINE=22687101; PubMed=12802337; DOI=10.1038/nature01705;
RA Yamauchi T., Kamon J., Ito Y., Tsuchida A., Yokomizo T., Kita S.,
Sugiyama T., Miyagishi M., Hara K., Tanoda M., Murakami K.,
Ohteki T., Uchida S., Takekawa S., Waki H., Tsuno N.H., Shibata Y.,
Terauchi Y., Froguel P., Tobe K., Koyasu S., Taira K., Kitamura T.,
Shimizu T., Nagai R., Kadowaki T.;

"Cloning of adiponectin receptors that mediate antidiabetic metabolic effects";
 Nature 423:762-769(2003).
 CC -1- FUNCTION: Receptor for globular and full-length adiponectin (APM1), an essential hormone secreted by adipocytes that acts as an antidiabetic. Probably involved in metabolic pathways that regulate lipid metabolism such as fatty acid oxidation. Mediates increased AMPK, PARAA ligand activity, fatty acid oxidation and glucose uptake by adiponectin. Has some high-affinity receptor for globular adiponectin but low-affinity receptor for full-length adiponectin.
 CC -1- SUBUNIT: May form homo and heteromultimers.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Localized to the cell membrane and intracellular organelles.
 CC -1- TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal muscle. Expressed at intermediate level in brain, heart, spleen, kidney, liver, placenta, lung and peripheral blood leukocytes.
 CC Weakly expressed in colon, thymus and small intestine.
 CC -1- SIMILARITY: Belongs to the ADIPOR family.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 369.

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 DR ENBL; AF151803; AAD34040.1; ALT FRAMES; mRNA.
 DR ENBL; BC001594; AAH01594.1; -; mRNA.
 DR ENBL; BC010743; AAH10743.1; -; mRNA.
 DR Ensembl; ENSG00000159346; Homo sapiens.
 DR HGNC; HGNC:24040; ADIPOR1.
 DR MIM; 607945; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0042562; P:hormone binding; IDA.
 DR GO; GO:0019395; P:fatty acid oxidation; IDA.
 DR GO; GO:0009755; P:hormone-mediated signaling; IDA.
 DR InterPro; IPR004254; HlyIII_related.
 DR Pfam; PF03006; HlyIII; 1.
 DR Fatty acid metabolism; Lipid metabolism; Receptor; Transmembrane.
 FT TOPO_DOM 1 136 Cytoplasmic (Potential).
 FT TRANSMEM 137 157 1 (Potential).
 FT TOPO_DOM 158 170 Extracellular (Potential).
 FT TRANSMEM 171 191 2 (Potential).
 FT TOPO_DOM 192 209 Cytoplasmic (Potential).
 FT TRANSMEM 210 230 3 (Potential).
 FT TOPO_DOM 231 235 Extracellular (Potential).
 FT TRANSMEM 236 256 4 (Potential).
 FT TOPO_DOM 257 267 Cytoplasmic (Potential).
 FT TRANSMEM 268 288 5 (Potential).
 FT TOPO_DOM 289 296 Extracellular (Potential).
 FT TRANSMEM 297 317 6 (Potential).
 FT TOPO_DOM 318 331 Cytoplasmic (Potential).
 FT TRANSMEM 332 352 7 (Potential).
 FT TOPO_DOM 353 375 Extracellular (Potential).
 SQ SEQUENCE 375 AA; 42616 MW; 1CC0300A7D178EB0 CRC64;
 Query Match 100.0%; Score 2009; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2e-154;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEBOQTCVPQBE 60
 DB 1 MSHKGSVVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEBOQTCVPQBE 60
 QY 61 EEEVRVLTPLQAHAMEKEEFVYKWEGRWRVDPYDVLDPWLKNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTPLQAHAMEKEEFVYKWEGRWRVDPYDVLDPWLKNDYLLHGHRRPMP 120
 QY 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTMRLPNMYFMAPLQEKVVFQGMFFLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTMRLPNMYFMAPLQEKVVFQGMFFLGA 180
 QY 181 VLCLSFWSLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFCSPQPLIYLS 240
 DB 181 VLCLSFWSLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFCSPQPLIYLS 240
 QY 241 IVCVLGISAIIVAOQWDREATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVVGOM 300
 DB 241 IVCVLGISAIIVAOQWDREATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVVGOM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 QY 361 FRYLEGSGCTDITLL 375
 DB 361 FRYLEGSGCTDITLL 375

RESULT 2

Q53YV6 HUMAN PRELIMINARY; PRT; 375 AA.
 AC Q53YV6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Progesterin and adipoQ receptor family member 1.
 GN Name=PAQR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tang Y.T., Hu T., Arterburn M., Boyle B., Bright J., Emtege P.,
 RA Funk W.;
 RT "PAQR proteins: a novel membrane receptor family defined by an ancient 7-transmembrane pass motif."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY424279; AAR08367.1; -; mRNA.
 KW Receptor.
 SQ SEQUENCE 375 AA; 42615 MW; 1CC0300A7D178EB0 CRC64;
 Query Match 100.0%; Score 2009; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2e-154;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEBOQTCVPQBE 60
 DB 1 MSHKGSVVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKAEBOQTCVPQBE 60
 QY 61 EEEVRVLTPLQAHAMEKEEFVYKWEGRWRVDPYDVLDPWLKNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTPLQAHAMEKEEFVYKWEGRWRVDPYDVLDPWLKNDYLLHGHRRPMP 120
 QY 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTMRLPNMYFMAPLQEKVVFQGMFFLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGFLVFLFLGILTMRLPNMYFMAPLQEKVVFQGMFFLGA 180
 QY 181 VLCLSFWSLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFCSPQPLIYLS 240
 DB 181 VLCLSFWSLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFCSPQPLIYLS 240
 QY 241 IVCVLGISAIIVAOQWDREATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVVGOM 300
 DB 241 IVCVLGISAIIVAOQWDREATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVVGOM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 QY 361 FRYLEGSGCTDITLL 375
 DB 361 FRYLEGSGCTDITLL 375

Db	241	IVCVLGISAI	IIVAQWDREATPKHRTQAGVFLGSLGSVPTMHFTTIAEGFVKATTVGQM	300
Qy	301	GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQI	FHVLVVAAAFVHFYGVSNLQE	360
Db	301	GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQI	FHVLVVAAAFVHFYGVSNLQE	360
Qy	361	FRYGLEGGCTDDTL	L 375	
Db	361	FRYGLEGGCTDDSL	L 375	
RESULT 5				
QSV9L5_PIG				
ID	QSV9L5_PIG	PRELIMINARY;	PRT;	375 AA.
AC	QSV9L5_PIG			
DT	01-FEB-2005	(T-REMBLrel. 29, Created)		
DT	01-FEB-2005	(T-REMBLrel. 29, Last sequence update)		
DE	01-FEB-2005	(T-REMBLrel. 29, Last annotation update)		
DE	Adiponectin receptor 1.			
OS	Sus scrofa (Pig)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;			
OC	Sus.			
NCBI_TaxID=9823;				
[1]				
RP	NUCLEOTIDE SEQUENCE.			
RP	PubMed=15542462;			
EX	Ding S.T., Liu B.H., Ko Y.H.;			
RT	"Cloning and expression of porcine adiponectin and adiponectin			
RT	receptor 1 and 2 genes in pigs."			
RT	J. Anim. Sci. 82:3162-3174(2004).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RP	Wang Y.C., Liu B.H., Ding S.T.;			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY578142; AAT72305.1; -; mRNA.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	InterPro; IPR004254; HlyIII_related.			
DR	Pfam; PF03006; HlyIII; 1.			
KW	Receptor.			
SEQ	SEQUENCE	375 AA; 42431 MW; 200C3C440883D662 CRC64;		
Query Match 97.4%; Score 1957; DB 2; Length 375;				
Best Local Similarity 97.3%; Pred. No. 3.3e-150;				
Matches 365; Conservative 2; Mismatches 8; Indels 0; Gaps 0				
Qy	1	MSHKGSVVAQNGAPAGNREADTVVLAELGPLLEERGRVIANPPKAEQEQTCPVQEE	60	
Db	1	MSHKGPGVGAQNGAPAGSREADTVVLAELGPLLEENGTRGTTNPPKAEQEACPVQEE	60	
Qy	61	ESEVRVLTPLOAHAMEKMEEFYKVGWEGRWRIPYDVL	PDMLKONDYLLHGHRRPMPES	120
Db	61	ESEVRVLTPLOAHAMEKMEEFYKVGWEGRWRIPYDVL	PDMLKONDYLLHGHRRPMPES	120
Qy	121	FRACFKSIPIRIHTETGNITWHLGLVPLFLFGIITMLRPNNYFWAPLQEKVFGMFFLGA	180	
Db	121	FRACFKSIPIRIHTETGNITWHLGLVPLFLFGIITMLRPNNYFWAPLQEKVFGMFFLGA	180	
Qy	181	VLCLSPSWLFHTVYCHSEKSVRSTFKLDYSGIALLIMGSPVPMLYTSFYCSPQRLIYLS	240	
Db	181	VLCLSPSWLFHTVYCHSEKSVRSTFKLDYSGIALLIMGSPVPMLYTSFYCSPQRLIYLS	240	
Qy	241	IVCVLGISAI	IIVAQWDREATPKHRTQAGVFLGSLGSVPTMHFTTIAEGFVKATTVGQM	300
Db	241	IVCVLGISAI	IIVAQWDREATPKHRTQAGVFLGSLGSVPTMHFTTIAEGFVKATTVGQM	300
Qy	301	GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQI	FHVLVVAAAFVHFYGVSNLQE	360
Db	301	GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQI	FHVLVVAAAFVHFYGVSNLQE	360
Qy	361	FRYGLEGGCTDDTL	L 375	

and mouse cDNA sequences.";
 [3]
 FUNCTION, AND TISSUE SPECIFICITY.
 MEDLINE-22687101; PubMed-12802337; DOI=10.1038/nature01705;
 Yamauchi T., Kamon J., Ito Y., Tsuchida A., Yokomizo T., Kita S.,
 Sugiyama T., Miyagishi M., Hara K., Tsunoda M., Murakami K.,
 Ohteki T., Uchida S., Takekawa S., Waki H., Tsuno N.H., Shibata Y.,
 Terauchi Y., Froguel P., Tobe K., Koyasu S., Taira K., Kitamura T.,
 Shimizu T., Nagai R., Kadowaki T.;
 "Cloning of adiponectin receptors that mediate antidiabetic metabolic
 effects.";
 Nature 423:762-769(2003).
 CC -!- FUNCTION: Receptor for globular and full-length adiponectin
 CC (APM1), an essential hormone secreted by adipocytes that acts as
 CC an antidiabetic. Probably involved in metabolic pathways that
 CC regulate lipid metabolism such as fatty acid oxidation. Mediates
 CC increased AMPK, PPARA ligand activity, fatty acid oxidation and
 CC glucose uptake by adiponectin. Has some high-affinity receptor for
 CC globular adiponectin but low-affinity receptor for full-length
 CC adiponectin.
 CC -!- SUBUNIT: May form homo and heteromultimers (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localized to the
 CC cell membrane and intracellular organelles (By similarity).
 CC -!- TISSUE SPECIFICITY: Widely expressed. Expressed in heart, kidney,
 CC liver, lung, skeletal muscle and spleen. Weakly expressed in brain
 CC and testis.
 CC -!- SIMILARITY: Belongs to the ADIPOR family.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a stop
 CC codon in position 353 which was translated as Tyr to extend the
 CC sequence and to a frameshift in position 375, which abolishes the
 CC stop codon.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AK012847; BAB28509.1; ALT_SEQ; mRNA.
 CC EMBL; BC014875; AHI4875.1; -; mRNA.
 CC Ensembl; ENSMUSG00000026457; Mus musculus.
 CC MGI; MGI:191924; Adipor1.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0042562; F:hormone binding; ISS.
 CC GO; GO:0046982; F:protein heterodimerization activity; IPI.
 CC GO; GO:0046982; F:protein self binding; IDA.
 CC GO; GO:0004872; F:receptor activity; IDA.
 CC GO; GO:0009755; P:hormone-mediated signaling; ISS.
 CC InterPro; IPR004254; HlyIII-related.
 CC Pfam; PF03006; HlyIII; 1.
 CC Fatty acid metabolism; Lipid metabolism; Receptor; Transmembrane.
 CC TOPO_DOM 1 136
 CC Transmem 137 157
 CC TOPO_DOM 158 170
 CC Transmem 171 191
 CC TOPO_DOM 192 209
 CC Transmem 210 230
 CC TOPO_DOM 231 235
 CC Transmem 236 256
 CC TOPO_DOM 257 267
 CC Transmem 268 288
 CC TOPO_DOM 289 296
 CC Transmem 297 317
 CC TOPO_DOM 318 331
 CC Transmem 332 352
 CC TOPO_DOM 353 375
 CC SEQUENCE 375 AA; 42366 MW; 0E72F81B5E9938CE CRC64;
 Query Match 97.3%; Score 1954; DB 1; Length 375;
 Best Local Similarity 96.8%; Pred. No. 5.8e-150;
 Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSSHKGSVVQAQNGAPASNRADTTVELAELGLPGLLEKGRVIANPPKAESEOTCPVQOE 60
 DB 1 MSSHKGSAQAQNGAPSGNRADTTVELAELGLPGLLEKGRASPPAKAEDQACPVQOE 60
 QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKVGWRVRVYPYDVLDPWLKXNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKVGWRVRVYPYDVLDPWLKXNDYLLHGHRRPMP 120
 QY 121 FRACFKSIFRIHTETGNIWTHLLGFLVFLFLGILTMLRPNMYFMAPLQEKVVGFMFFLGA 180
 DB 121 FRACFKSIFRIHTETGNIWTHLLGFLVFLFLGILTMLRPNMYFMAPLQEKVVGFMFFLGA 180
 QY 181 VLCLFSWLFHTVYCHSEKVSRTFSLDYSGLIALLMGSFVPLWLYSPYCSQPRLLIYL 240
 DB 181 VLCLFSWLFHTVYCHSEKVSRTFSLDYSGLIALLMGSFVPLWLYSPYCSQPRLLIYL 240
 QY 241 IVCVLIGISAIIVAQNDREATPKHROTTRAGVFLGILGSLGVPTMHTTIAEGFVKATTVGQM 300
 DB 241 IVCVLIGISAIIVAQNDREATPKHROTTRAGVFLGILGSLGVPTMHTTIAEGFVKATTVGQM 300
 QY 301 GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 DB 301 GNFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 QY 361 FRYGLEGGCTDITLL 375
 DB 361 FRYGLEGGCTDITLL 375
 RESULT 7
 Q53Y4 MOUSE PRELIMINARY; PRT; 375 AA.
 AC Q53Y4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Progestin and adiponectin receptor family member 1.
 GN Name=Adipor1; Synonyms=Paqr1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Tang Y.T., Hu T., Arterburn M., Boyle B., Bright J., Emtage P.,
 RA Funk W.;
 RT "PAQR proteins: a novel membrane receptor family defined by an ancient
 RT 7-transmembrane pass motif.";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY424290; AAR08378.1; -; mRNA.
 DR MGI; MGI:191924; Adipor1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0046982; F:protein heterodimerization activity; IPI.
 DR GO; GO:0042802; F:protein self binding; IDA.
 DR GO; GO:0004872; F:receptor activity; IDA.
 DR GO; GO:0019395; P:fatty acid oxidation; IDA.
 DR Receptor.
 KW SEQUENCE 375 AA; 42366 MW; 0E72F81B5E9938CE CRC64;
 Query Match 97.3%; Score 1954; DB 2; Length 375;
 Best Local Similarity 96.8%; Pred. No. 5.8e-150;
 Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MSSHKGSVVQAQNGAPASNRADTTVELAELGLPGLLEKGRVIANPPKAESEOTCPVQOE 60
 DB 1 MSSHKGSAQAQNGAPSGNRADTTVELAELGLPGLLEKGRASPPAKAEDQACPVQOE 60
 QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKVGWRVRVYPYDVLDPWLKXNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKVGWRVRVYPYDVLDPWLKXNDYLLHGHRRPMP 120

QY 121 FRACFKSIPIRIHTETGNIWTHLLGFLVFLPLGLTLMLRPNMYFMAPLQKVVFGMPFLGA 180
DB 121 FRACFKSIPIRIHTETGNIWTHLLGFLVFLPLGLTLMLRPNMYFMAPLQKVVFGMPFLGA 180
QY 181 VCLCSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYLS 240
DB 181 VCLCSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYLS 240
QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQM 300
DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQM 300
QY 301 GWFFLMAVMTIAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 360
DB 301 GWFFLMAVMTIAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 360
QY 361 FRYGLEGGCTDDTL 375
DB 361 FRYGLEGGCTDDSL 375

RESULT 8

Q6SQ15_PIG PRELIMINARY; PRT; 348 AA.
ID O6SQ15_PIG
AC O6SQ15_PIG
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Adiponectin receptor 1 (Fragment).
GN Name=ADIPOR1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15705753;
RA Lord E., Ledoux S., Murphy B.D., Beaudry D., Palin M.P.;
RT "Expression of adiponectin and its receptors in swine.";
RL J. Anim. Sci. 83:565-578(2005).
DR EMBL: AV452710; AAR91794.1; -; mRNA.
DR GO: GO:0016021; C-integral to membrane; IEA.
DR GO: GO:0004872; F-receptor activity; IEA.
DR InterPro: IPR004254; HlyIII-related.
DR Pfam: PF03006; HlyIII; 1.
FT NON_TER 1
FT NON_TER 348 348
SQ SEQUENCE 348 AA; 39899 MW; 0CE2DF4F7DE6F4F8 CRC64;

Query Match 91.7%; Score 1842; DB 2; Length 348;

Best Local Similarity 98.3%; Pred. No. 6.5e-141;

Matches 342; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 27 LAELGPLLEKGRVIANPPKABEEQTCVPQEESEVRVLTLPLOAHAMEKMEEFVYK 86
DB 1 LAELGPLLEKGRGTNTNPPKABEEQACVPQEESEVRVLTLPLOAHAMEKMEEFVYK 60
QY 87 VNEGRWRVIPYDVLPMKNDYLLHGRHPMPSPRACFKSIFRIHTETGNIWTHLLGFV 146
DB 61 VNEGRWRVIPYDVLPMKNDYLLHGRHPMPSPRACFKSIFRIHTETGNIWTHLLGFV 120
QY 147 LFLFLGLTLMLRNMYFMAPLQKVVFGMPFLGLVCLSLFHTVYCHSEKVSRTFSK 206
DB 121 LFLFLGLTLMLRNMYFMAPLQKVVFGMPFLGLVCLSLFHTVYCHSEKVSRTFSK 180
QY 207 LDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYLSIVCVLGISAIIVAQWDRFATPKHQ 266
DB 181 LDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYLSIVCVLGISAIIVAQWDRFATPKHQ 240
QY 267 RAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQMGWFFLMAVMTIAGLYAARIPIRPF 326

DB 241 RAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQMGWFFLMAVMTIAGLYAARIPIRPF 300
QY 327 PKGPDINWQSHQIHVLVVAFAAFVHFYGVSNLQBFYRLEGCTDDTL 374
DB 301 PKGPDINWQSHQIHVLVVAFAAFVHFYGVSNLQBFYRLEGCTDDTL 348

RESULT 9

Q4PKP2_CHICK PRELIMINARY; PRT; 375 AA.
ID Q4PKP2_CHICK
AC Q4PKP2;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Adiponectin receptor 1.
GN Name=ADIPOR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hyline W36; TISSUE=Adipose tissue;
RA Ramachandran R., Ocon O., Metzger S.;
RT "Molecular Cloning and Tissue Expression of Chicken AdipoR1 and
RT AdipoR2 cDNA.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: DQ072275; AAY81969.1; -; mRNA.
KW Receptor.
SQ SEQUENCE 375 AA; 42182 MW; 6ACBA83D24771F00 CRC64;

Query Match 90.4%; Score 1817; DB 2; Length 375;

Best Local Similarity 91.2%; Pred. No. 7.5e-139;

Matches 343; Conservative 11; Mismatches 20; Indels 2; Gaps 2;

QY 1 MSSHKGSVVAQNGAPASNREADTVLAEALGPLLEKGRVIANPPKABEEQTCVPQEE 60
DB 1 MASRKAAAAGNGLAAGRDRHAHLAEALGPLLEKGEQGNAGTASA-EDPPCPVAREE 59
QY 61 EEE-VRVLTLPLOAHAMEKMEEFVYKVGGRWRVIPYDVLPMKNDYLLHGRHPMP 119
DB 60 EEEVVRVLTLPLOAHAMEKMEEFVYKVGGRWRVIPYDVLPMKNDYLLHGRHPMP 119
QY 120 SFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLTLMLRPNMYFMAPLQKVVFGMPFLG 179
DB 120 SFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLTLMLRPNMYFMAPLQKVVFGMPFLG 179
QY 180 AVLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYL 239
DB 180 AVLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSQPRLIYL 239
QY 240 SIVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQ 299
DB 240 SIVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPMTMHTIAGGFVKATTVGQ 299
QY 300 MGWFFLMAVMTIAGLYAARIPIRPFPGKEDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 359
DB 300 MGWFFLMAVMTIAGLYAARIPIRPFPGKEDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 359
QY 360 EFRYGLEGGCTDDTL 375
DB 360 EFRYGLEGGCTDDSL 375

RESULT 10

Q50100_XENLA PRELIMINARY; PRT; 384 AA.
ID Q50100_XENLA
AC Q50100;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RG NIH MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC044388; AAH44388.1; -; mRNA.
DR Ensembl; ENSDARG0000042717; Danio rerio.
DR ZFIN; ZDB-GENE-040426-2896; adiporib.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR Pfam; PF03006; HlyIII; 1.
KW Receptor.
SQ SEQUENCE 377 AA; 42426 MW; D85C91CD603B19EC CRC64;

Query Match 79.9%; Score 1604.5; DB 2; Length 377;
Best Local Similarity 78.1%; Pred. No. 1.3e-121;
Matches 299; Conservative 29; Mismatches 34; Indels 21; Gaps 4;

QY 4 HKGSVVAQNGAPASNPREAD-----TVELAELGPLL-----BEKGRVIANPPKAEERQ 52
DB 5 HHGDC---GSNSDAERRATDDEANMEDAELSELGPLTSPANSEEGSGASPDENEDE- 60

QY 53 TCPVPOEEBEVRVLTLPLOAHAMEKMEEFVYKVGWGRWVPIYDVLDPWLKNDNDYLLH 112
DB 61 -----KEEGRLRVVLTLPLOAHAMEKMEEFVHKIWEGRWVPIYHLLPDLKNDNDYLLH 114

QY 113 GHRPPMPFRACFKSIPIRIHTETGNIWTHLLGFLFLGLGILTLMLRPNMYFMAPLOEKVV 172
DB 115 GHRPPMPFRACFKSIPIRIHTETGNIWTHLLGFLGLGILTLMLRPNMYFMAPLOEKVV 174

QY 173 FGMPFLGAVCLSPSWLPHYVCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYCSP 232
DB 175 FGVPFLGAVCLSPSWLPHYVCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYCSP 234

QY 233 QPRLIYLSIVCVLGISALIIAQNDRFATPKHROTFRAGVFLGLSGVVPVTHFTIABGFV 292
DB 235 QPRLIYLSVVCVLGVAALIIAQNDRFATPKHROTFRAGVFLGLSGVVPVTHFTIABGFV 294

QY 293 KATTVGQMGWFFLMVAVYITGAGLYAARIPIERFPFGKFDIWFQSHQIFHVLVVAAPVHF 352
DB 295 KATTVGQMGWFFLMVAVYITGAGLYAARIPIERFPFGKFDIWFQSHQIFHVLVVAAPVHF 354

QY 353 YGVSNLOEFYRGLGGCTDITLL 375
DB 355 YGIVSNLOEFYRGLGGCTDITLL 377

RESULT 14
Q4SS53 TETNG PRELIMINARY; PRT; 318 AA.
AC Q4SS53;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCAF14479, whole genome shotgun sequence.
GN (Fragment).
GN ORFNames=GSTENG0013607001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dagilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier C., Couancanau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet P., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
FT EMBL; CAEE01014479; CAF96529.1; -; Genomic_DNA.
FR NON TER 1
SQ SEQUENCE 318 AA; 36444 MW; C18F0ACFBEE28470 CRC64;

Query Match 78.3%; Score 1573; DB 2; Length 318;
Best Local Similarity 89.3%; Pred. No. 3.8e-119;
Matches 284; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 58 QBESEVRVLTLPLOAHAMEKMEEFVYKVGWGRWVPIYDVLDPWLKNDNDYLLHGRPP 117
DB 1 EDDDEVAEVLTLPLQAHAMEKMEEFVHKVWGRWVPIFFHVLPEWLKNDNDYLLHGRPP 60

QY 118 MPFRACFKSIPIRIHTETGNIWTHLLGFLFLGLGILTLMLRPNMYFMAPLOEKVFGMPF 177
DB 61 MPFRACFKSIPIRIHTETGNIWTHLLGFLGLGILTLMLRPNMYFMAPLOEKVFGMPF 120

QY 178 LGAVLCLSPSWLPHYVCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYCSPRLI 237
DB 121 LGAVLCLSPSWLPHYVCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYCSPRLI 180

QY 238 YLSIVCVLGISALIIAQNDRFATPKHROTFRAGVFLGLSGVVPVTHFTIABGFVXATTV 297
DB 181 YLSIVCVLGISALIIAQNDRFATPKHROTFRAGVFLGLSGVVPVTHFTIABGFVXATTV 240

QY 298 GQMGWFFLMVAVYITGAGLYAARIPIERFPFGKFDIWFQSHQIFHVLVVAAPVHFVGSN 357
DB 241 GQMGWFFLMVAVYITGAGLYAARIPIERFPFGKFDIWFQSHQIFHVLVVAAPVHFVGSN 300

QY 358 LOEFYRGLGGCTDITLL 375
DB 301 LOEFYRGLGGCTDITLL 318

RESULT 15
Q6KSS5_XENLA PRELIMINARY; PRT; 385 AA.
AC Q6KSS5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC85478 protein.
GN Name=MGC85478;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RN Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	409	20.4	352	2	US-09-248-796A-16098	Sequence 16098, A
2	164	8.2	199	2	US-10-104-047-2886	Sequence 2886, A
3	152	7.6	224	2	US-09-902-540-14719	Sequence 14719, A
4	151.5	7.5	228	2	US-09-252-991A-36973	Sequence 36973, A
5	129	6.4	143	2	US-09-270-767-46435	Sequence 46435, A
6	122	6.1	234	2	US-09-107-532A-4817	Sequence 4817, A
7	118.5	5.9	236	2	US-09-134-000C-3636	Sequence 3636, A
8	114.5	5.7	227	2	US-09-134-001C-4836	Sequence 4836, A
9	114.5	5.7	227	2	US-09-710-279-2642	Sequence 2642, A
10	108	5.4	245	2	US-09-248-796A-16029	Sequence 16029, A
11	106.5	5.3	231	2	US-09-489-039A-11927	Sequence 11927, A
12	106	5.3	272	2	US-09-902-540-14983	Sequence 14983, A
13	105	5.2	215	2	US-09-583-110-3435	Sequence 3435, A
14	105	5.2	233	2	US-09-107-433A-2676	Sequence 2676, A
15	104	5.2	722	2	US-09-489-039A-8942	Sequence 8942, A
16	103.5	5.2	234	2	US-09-270-767-44557	Sequence 44557, A
17	102.5	5.1	625	2	US-08-959-004-10	Sequence 10, A
18	102	5.1	142	2	US-09-902-540-13948	Sequence 13948, A
19	101	5.0	224	2	US-09-252-991A-16953	Sequence 16953, A
20	100.5	5.0	354	2	US-09-583-110-4997	Sequence 4997, A
21	100.5	5.0	325	2	US-09-107-433A-2619	Sequence 2619, A
22	99.5	5.0	525	2	US-09-252-991A-27543	Sequence 27543, A
23	99	4.9	218	2	US-09-328-353-5215	Sequence 5215, A
24	97	4.8	499	2	US-09-540-236-3217	Sequence 3217, A
25	96.5	4.8	346	2	US-09-710-279-504	Sequence 504, A
26	96.5	4.8	383	2	US-09-710-279-2026	Sequence 2026, A
27	96.5	4.8	503	2	US-09-134-001C-3096	Sequence 3096, A

```

; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2886
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2886

Query Match      8.2%; Score 164; DB 2; Length 199;
Best Local Similarity 22.8%; Pred. No. 2.5e-09;
Matches 60; Conservative 31; Mismatches 86; Indels 86; Gaps 7;

QY 93 RVIPYDVLDMKNDYLLHGRPPMPSPFRACPKSIFRIHTETGNTWTHLLGVLFPLG 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 RLDMWASSPHLQFNKFLVTGYR-PASSGGCLRSFLYHNLGNLYAH-----G 56

QY 153 ILTMLRPNMYFMAPLOEKVVGFMFFLGVLCLSFSLFHTVYCHSEKVSRTSKLDYSGI 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ALPIIHCTACRPLWLRPTALGVTVLSGVA-----GMRALTAPSTSA RL-RAFGW--QAAA 109

QY 213 ALLIMGSFVPMWLYSYFYSPQPRLIYLSIVCVLIGISAIIVAOQDRPATPKRQTRAGVFL 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 RLLVFGA-----RGVGL 121

QY 273 GGLSGVPMHTIAEGFVKATTVGQMGWFFLMVAVYITGAGLYAARIPERFPFGKFDI 332
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 GSGAPGSLPC-----YLRMDALALLGGVNVNVARLPERMGPGRFDY 161

QY 333 WFQSHQIFHVLVVAAPVHFYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 162 WGNSHQIMHLLSVGSILQLHAGV 184

RESULT 3
US-09-902-540-14719
; Sequence 14719, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14719
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-14719

Query Match      7.6%; Score 152; DB 2; Length 224;
Best Local Similarity 27.9%; Pred. No. 5.9e-08;
Matches 60; Conservative 29; Mismatches 100; Indels 26; Gaps 8;

QY 140 THLLGVFLFLGILTMWRP--NMVFMAPLOEKVVGFMFFLGVLCLSFSLFHTVYCHS 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 SHAVAFVAALLGCIQLALMPVRGPQYLADL-----VFGG---SMVLMFGVSATYHR-FTWG 75

QY 198 EKVSRTFSKLDYSGLIIMGSFVPMWLYSYFYSPQPRLIYLSIVCVLIGISAIIVAOQDR 257

```

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Db 76 MDAYRRIQRFDAIYVILIAGSFTPMATLDTTGTSLYLLWL-----MMIAALTGAGLTL 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 FATPKHQTRAGVFLGILSGVVPVPMHTIAEGFVKATTVGQMGWFFLMVAVYITGAGLY 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 LGVHTSRGLRSALYVALG--AVATPVMLRLPE-----VTGSGRVAVLVLGGVLIYAVGAVIY 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 AARIPEFPFGKFDIWFQSHQIFHVLVVAAPVHF 352
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 ARR-----WPDPIPTVFGYHEIFHLLVVAAGVHY 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-252-991A-26973
; Sequence 26973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26973
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26973

Query Match      7.5%; Score 151.5; DB 2; Length 228;
Best Local Similarity 24.6%; Pred. No. 6.9e-08;
Matches 62; Conservative 36; Mismatches 87; Indels 67; Gaps 11;

QY 132 HTETGNIWTHLLGFVL-----FLFLGILTMLRNMYFMAPLOEKVV-FGMFFLGVLCLSF 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 HGERLNWATHLIGAVAACTGAVMLTVQASLNGSPW-----KIVGVGVYGTLLLYSI 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 187 SWLPHTVYCHSEKVSRTFSKLDYSGLIIMGSFVPMWLYSYFYSPQPRLIYLSIVCVLG 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 STAYHSVGRAKVVR-----KLDHLSIYLLIAGSYTP-----FC-----LVTLRG 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 247 ISAIIVAOQDRPATPKRQTRAGVFLGILSGVVPVPMHTIAEGFVKATTVGQMGWFFLM 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 -----PWG-----WTLFGIVWGLAVLGMLOEIKPRSEARVLSVVIVAVMGWIVLI 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 307 AVMYI-----TGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFY 353
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 AVKPLAALGAGFTWLAAGVLYTVGIVFYAIDHRFRHW-----HGIWHLFVIAGSLHFPV 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 354 GVSNLQEFYGL 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 AI-----WRYVL 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-270-767-46435
; Sequence 46435, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7325-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46435
; LENGTH: 143

```

```

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46435

Query Match
Best Local Similarity 6.4%; Score 129; DB 2; Length 143;
Matches 36; Conservative 21; Mismatches 47; Indels 28; Gaps 5;

QY 223 WLYYSPFCSPQRLIYLSIVCVLIGISAIIVAQ--WDR---FATPKHQTRAGVFLGLGLS 277
DB 1 WLIIVSYC-----VLSLNGLYKALTASSPQRRCLFALPPAWRS---ILTLRLR 47

QY 278 GVVPTMHTTIAEGFVKATTVGQMGWFLMAVMYITGAGLYAARIPERFPFGKFDIWFQSH 337
DB 48 GMVGGSHMALSHVYLQVEVDG-----VSILGGAIGAMRIPEKWFPGVVDVFLNSH 97

QY 338 QIFHVLVVAAP 349
DB 98 NIMHVLVVAVY 109

RESULT 6
US-09-107-532A-4817
; Sequence 4817, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Walham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 4817:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...234
; SEQUENCE DESCRIPTION: SEQ ID NO: 4817:
US-09-107-532A-4817

Query Match
6.1%; Score 122; DB 2; Length 234;

```

```

Best Local Similarity 24.1%; Pred. No. 0.00011;
Matches 59; Conservative 47; Mismatches 83; Indels 56; Gaps 15;

QY 125 FKSIFRIHTETGNIWTHLGLFVLFLGILTLMLRPNMYPMAFLQEKVFGMPFLGAVLCL 184
DB 23 FNRITVEILNEVENAVTHGIGTGLSI-AGLVLLVKGAGHLHSLH---IVSYAIYSGMMIL 78

QY 185 SP--SWLFHT-VYCHSEKVSRTFSKLDYSGIALLMGSFVP-----WLYYSPFCSPQ 233
DB 79 LFLTSTLFLHSLIFTAKKVQVF---DHSSIFLLIAGSYTPFCLLSIRGMLGWTLP---- 131

QY 234 PRLIYLSIVCVLGI--SAIIAQMWRFPATPKHQTRAGVFLG-LGLSGVVPTMHTFTIAGS 290
DB 132 ---VLIMLPAIIIGIYKALTLLHRRKRSKV---STIIYFMGLWCVAAPVLYH----- 179

QY 291 FVKATTVGOMGWFFLMA--VMYITGAGLYAARIPERFPFGKFDIWFQSHOIFHVLV-VAA 347
DB 180 -----SLGWTGVILMVAGGLSYTICA-----FPYSLNSIRYM-HVWVHLFVMLGA 223

QY 348 AFVHF 352
DB 224 GMYF 228

```

```

RESULT 7
US-09-134-000C-3636
; Sequence 3636, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3636
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3636

```

```

Query Match
Best Local Similarity 5.9%; Score 118.5; DB 2; Length 236;
Matches 56; Conservative 42; Mismatches 92; Indels 49; Gaps 11;

QY 125 FKSIFRIHTETGNIWTHLGLFVLFLGILTLMLRPNMYPMAFLQEKVFGMPFLGAVLCL 184
DB 24 FSKKYLIVNEVLNAVTHGIGAGLSI-AGLVILLVKGARLGSPIH---VVSYAIYSGMLIL 79

QY 185 SP--SWLFHT-VYCHSEKVSRTFSKLDYSGIALLMGSFVP-----WLYYSPFCSPQ 233
DB 80 LFLSSTLFLHSLIFTAKKVQVF---DHSSIFLLIAGSYTPFCLLSIRGMLGWTLP---- 132

QY 234 PRLIYLSIVCVLGISAIIVAQWDRFPATPKHQTRAGVFLGSLSGVVPTMHTFTIAGSFVK 293
DB 133 -----SLVWLIAIVGIVYKSLTLHKQETVKNIISTIIYIVLWLCIIAARPLYESLGT- 185

QY 294 ATTVGOMGWFFLMA--VMYITGAGLYAARIPERFPFGKFDIWFQSHOIFHVLVVAAPV 350
DB 186 -----GTALLVAGGVSVTLGAAPFYSLK-----NVRPM-HVWVHLFVMLAAIL 226

```

```

RESULT 8
US-09-134-001C-4836
; Sequence 4836, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

```



```

QY 129 FRIHTETGNIWTHLLGFLVFLFLGILMLRPNMYFMAPLOEKVVGFMFLGAVLCLFSW 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 YSLAEVANSISHGIGLV-FGIVGLVLLVQAADTNASATAIASYSLYGGSMIMFLAST 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 LFTVYCHSEKRTFSKLDYSGIALLIMSGFVPMLYYFCSPQPRLLIVLSIVCVLGIS 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 LYHAI--PHORAKQWLKFDHCAIYLLIAGTYTFFL-----LVGLNSPLAKGLM 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 AIIVAOWDRPATPKHRQTRAGVFLGLSGVPMTHFTIAEGF--VKATTVGQMGWFFLM 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 IVI--W-----SLALLGIL--FKLTIAHREKILSLVLYLTWGLSLI 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 -----AVMYITGAGLYAA-RIPERFFPKGDIWFQSHQIFHVLVV 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 VYQLAVKLVAGVGTLLAVGGVYSLGVIFVCKRIP-----YNHAIWGHFVL 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 AAAPVHFYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 GGSVCHFLAI 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12

US-09-902-540-14983
; Sequence 14983, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14983
; LENGTH: 571
; TYPE: PRF
; ORGANISM: Myxococcus xanthus
US-09-902-540-14983

Query Match 5.3%; Score 106; DB 2; Length 571;

Best Local Similarity 24.4%; Pred. No. 0.022;
Matches 48; Conservative 32; Mismatches 69; Indels 48; Gaps 11;

```

QY 125 FKSIFRI-HTETGNIWTHLLGFLVFLFLGILT-----MLRPNMYFMAPLOEK--VVFQMF 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 FNSVHSFTQSDIGTFLVFLGLVLCVGLLAVRGPLLVPEGLASPLSREASILVNNLV 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 FLGAVLCLFSWLFHTVY-----CHSEKYS---RTFSKLDY-SGIALLIM--GSPVPW 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 F-----VAITFTVLLGLTYPLIASEAVHGVRSVSGSEPFYFNKMAVPGGIAVLFLMGVPLPW 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 LYYSFCSPQPRLLIVLSIVCVLGISAIIVAOWDRFATPKHRQTRAGVFLGLSGVVPFM 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 -----GKPDPAUURRQFIPIPSVGLVVT-----ACFAVGLRGVYPLM 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 284 HFTIAEGFVKATTVGOM 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 TFGLA-GFVTVTVREL 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13

US-09-583-110-3435
; Sequence 3435, Application US/09583110
; Patent No. 6699703

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

```

; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3435
; LENGTH: 215
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3435

Query Match 5.2%; Score 105; DB 2; Length 215;
Best Local Similarity 20.1%; Pred. No. 0.0066;
Matches 52; Conservative 38; Mismatches 69; Indels 100; Gaps 13;

QY 134 ETGNIWTHLLGFLVFLFL-----GILTMLRPNMYFMAPLOEKVVGFMFLGAV 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 ETANSVTHAVGAVIMLILLPISSIYSYEAHGFSSIGVSIF-----V 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LCLFSFWLFHTVYCHSEKVSRTFSK-----LDYSGIALLIMSGFVP-----WLYYSFY 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 ISLFLMFLSSTIY-HSMAYGSTHKYVLRIDHSMIYVAIAGSYTPVVLTMNNWFGY--- 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 CSPQPRLLIVLSIVCVLGISAIIVAOWDR-----FATPKHRQTRAGVFLGLG--LSG 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 -----LIIVIHWGTTFITGLTKIFAINVNDKESLALYLMGWLVA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 VVPTMHFTTIAEGFVKATTVGQMGWFFLM--AVMYITGAGLYAARIPEFPFGKFDIWFQS 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 155 IIPAI-----INOTT--PVFWSLMVATGGLCYTVGAGFYAKKDP--YF----- 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 HQIFHVLVVAAAPVHFYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 HMIWHLFIILAAVSLQYIAI 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

US-09-107-433-2676
; Sequence 2676, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSER: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

```

;
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-011
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 2676:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;   ORGANISM: Streptococcus pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...233
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2676:
US-09-107-433-2676

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Query Match 5.2%; Score 105; DB 2; Length 233;
Best Local Similarity 20.1%; Pred. No. 0.0074;
Matches 52; Conservative 38; Mismatches 69; Indels 100; Gaps 13;

```

QY 134 ETGNIWTHLGLFVFLFLP-----GILTMLRPNMYFWAPLQEKVVGCMFFLGAV 181
DB 34 EIANSVTHAVGAVIMILLIPSIISYEAHGLSSIGVSIP-----V 75

QY 182 LCLSPSWLPHTVYCHSEKVSRTFSK----LDYSGIALLIMSGFVP-----WLYYSFY 229
DB 76 ISLFLMPLSSTIY-HSMAYGSKYVLRIDHSMIYVAIAGSYTPVVVLTLMNNWFGY--- 131

QY 230 CSPQPLIYLSIVCVLGISAIIVQWDR-----FATPKHQRTAGVFLGLG---LSG 278
DB 132 -----LIIVIHMGTTIFGTLYKIFAINVNDKFSLALYLMGWVLA 172

QY 279 VVPTMHTTIAEGFVKATTVGCMGFPLM--AVMYITGAGLYAARIPEPFPGKFDIWFOS 336
DB 173 IIPAI-----INQTT--PVFWSLMVTGGLCYTVGAGFYAKKP--YF----- 210

QY 337 HQIFHVLVVAAFVHFYGV 355
DB 211 HMIWHLFILAASVLQYIAI 229

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RESULT 15
US-09-489-039A-8942
; Sequence 8942, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8942
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8942

Query Match 5.2%; Score 104; DB 2; Length 722;
Best Local Similarity 23.5%; Pred. No. 0.052;
Matches 77; Conservative 43; Mismatches 123; Indels 84; Gaps 16;

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QY 63 EVKVLTLPLQAHAMKMEEFYKVGWRVRVIPPYDVLDPW-----LKN--DYLLHGR 115
DB 228 EVSVIGIVL-----LVASIWFG--GVIAHD--PYWGPALTFKDTTITTLIGY- 271

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Search completed: April 19, 2006, 14:04:35
Job time : 38.2774 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rapn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 19, 2006, 14:20:09 ; Search time 20.5861 Seconds
(without alignments)
801.567 Million cell updates/sec

Title: US-10-799-943-2
Perfect score: 2009
Sequence: 1 MSHKGSVVAQNGAPASNR.....SNLQEPFRYGLGGCTDDTL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 4402918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /SIDSS5/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
6: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	29.6	318	7 US-11-188-298-16712	Sequence 16712, A
2	530.5	26.4	324	7 US-11-188-298-7728	Sequence 7728, Ap
3	515	25.6	315	7 US-11-188-298-6654	Sequence 6654, Ap
4	479.5	23.9	376	7 US-11-096-568A-11895	Sequence 11895, A
5	479.5	23.9	406	7 US-11-096-568A-11894	Sequence 11894, A
6	479	23.8	329	7 US-11-188-298-17246	Sequence 17246, A
7	477	23.7	324	7 US-11-096-568A-17089	Sequence 17089, A
8	477	23.7	345	7 US-11-096-568A-17088	Sequence 17088, A
9	477	23.7	371	7 US-11-096-568A-17087	Sequence 17087, A
10	474	23.6	317	7 US-11-188-298-21152	Sequence 21152, A
11	474	23.6	327	7 US-11-188-298-7868	Sequence 7868, Ap
12	468	23.3	328	7 US-11-188-298-13492	Sequence 13492, A
13	453.5	22.6	380	7 US-11-096-568A-22007	Sequence 22007, A
14	453.5	22.6	426	7 US-11-096-568A-22006	Sequence 22006, A
15	451.5	22.5	332	7 US-11-188-298-326	Sequence 326, App
16	445	22.2	263	7 US-11-188-298-15865	Sequence 15865, A
17	437	21.8	387	7 US-11-096-568A-27407	Sequence 27407, A
18	437	21.8	405	7 US-11-096-568A-27406	Sequence 27406, A
19	431	21.5	374	7 US-11-096-568A-27408	Sequence 27408, A
20	425	21.2	317	7 US-11-188-298-15303	Sequence 15303, A
21	416.5	20.7	351	7 US-11-096-568A-26845	Sequence 26845, A
22	407	20.3	316	7 US-11-188-298-12382	Sequence 12382, A
23	399	19.9	316	7 US-11-188-298-9290	Sequence 9290, Ap
24	377	18.8	497	7 US-11-188-298-2733	Sequence 2733, Ap
25	373.5	18.6	215	7 US-11-096-568A-26847	Sequence 26847, A

26	373.5	18.6	252	7 US-11-096-568A-26846	Sequence 26846, A
27	372	18.5	442	7 US-11-188-298-13605	Sequence 13605, A
28	357	17.8	221	7 US-11-096-568A-22008	Sequence 22008, A
29	356	17.7	498	7 US-11-188-298-1166	Sequence 1166, Ap
30	336.5	16.7	490	7 US-11-188-298-2544	Sequence 2544, Ap
31	318.5	15.9	822	7 US-11-188-298-6572	Sequence 6572, Ap
32	269	13.4	467	7 US-11-096-568A-19600	Sequence 19600, A
33	269	13.4	476	7 US-11-096-568A-19599	Sequence 19599, A
34	261	13.0	401	7 US-11-096-568A-19601	Sequence 19601, A
35	252	12.5	419	7 US-11-188-298-1381	Sequence 1381, Ap
36	251	12.5	543	7 US-11-188-298-21359	Sequence 21359, A
37	204.5	10.2	346	5 US-09-978-360A-537	Sequence 537, App
38	176	8.8	137	6 US-10-644-807-409	Sequence 409, App
39	164	8.2	199	7 US-11-072-512-2886	Sequence 2886, Ap
40	137.5	6.8	210	7 US-11-045-004-1082	Sequence 1082, Ap
41	114.5	5.7	227	6 US-10-793-626-2642	Sequence 2642, Ap
42	111.5	5.6	354	7 US-11-188-298-13845	Sequence 13845, A
43	107.5	5.4	448	7 US-11-087-099-10069	Sequence 10069, A
44	100.5	5.0	464	7 US-11-087-099-8095	Sequence 8095, Ap
45	100	5.0	258	7 US-11-096-568A-30003	Sequence 30003, A

ALIGNMENTS

RESULT 1

US-11-188-298-16712
; Sequence 16712, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Aabad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USSES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16712
; LENGTH: 318
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-16712

Query Match 29.6%; Score 595; DB 7; Length 318;

Best Local Similarity 43.0%; Pred. No. 1e-45;

Matches 122; Conservative 46; Mismatches 102; Indels 14; Gaps 4;

Qy	94	VIPYDVLDPWLKNDVLLHGRPPMPSFRACFKSIFRIHTETGNIWTHLLGFLFLGLI	153
Db	39	LVMHDELPHWQRDNQIHITGYRPASYSFRGSFQSILYIHNETVNIYTHLLPSVLAIPAAI	98
Qy	154	LTLRLPNMY-FWAPLOEKV-----VGFMEFLGAVLCLSFSLFHTVYCHSEKVSRTFSK	206
Db	99	-----OLRALAPRYETATDGIAPGCFVGAALCLGMSAFYHTISNHSPTVARIGNT	152
Qy	207	LDYSGIALIMSGFEVFWLYSYFCSPQRLIYLISIVCVLGISAIIVQWDRFATPKHQRT	266
Db	153	FDYIGIVGLGVGSFVSFVYGYFCVPELQRLYWSMCTIGLGCIVVSIRPKFTRPRWF	212
Qy	267	RAGVFGLGLSGVVPMTHTFIAGFVKATVVGOMGHFFLMVNMVITGAGLYAARIPRPF	326
Db	213	RAAMFVGMGLSAFVFPVVHGLYGRDQMMRQIGLGLLQGLFYILGAGIYAARVPERLR	272
Qy	327	PGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEERY-GLEGGC	369
Db	273	PGGFDLWGSSHQIFHVLVWCAVAHUTGLLRAPDFRHNHTAGSC	316

RESULT 2

US-11-188-298-7728
; Sequence 7728, Application US/11188298
; Publication No. US20060075522A1

